CONTEMPORARY STOCK STRUCTURE OF MUSKELLUNGE POPULATIONS IN NORTHERN WISCONSIN

by

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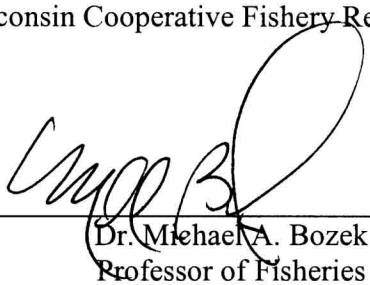

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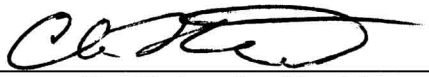

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ABSTRACT

Wisconsin has more than 700 muskellunge (*Esox masquinongy*) populations providing a diverse array of angling experiences from high-density action waters to low-density trophy fisheries. The Wisconsin Department of Natural Resources' (WDNR) muskellunge management goals include maximizing angling opportunities while preserving genetic integrity. The WDNR manages muskellunge populations through regulations, such as daily bag limits and length limits, and a prolific stocking program. Supplemental stocking can have strong impacts on the genetic integrity of any population. The WDNR currently delineates muskellunge management units based on watershed boundaries. The goal of this study was to resolve the genetic structure of native muskellunge populations in northern Wisconsin. Specifically, the objective was to delineate and compare contemporary genetic structure and current management units to determine if they were congruent. Non-lethal fin clips from 43 naturally recruiting populations ($n \approx 50$/population) across the native range of muskellunge in Wisconsin were collected. Samples were genotyped using a suite of 14 microsatellite loci. Bayesian analysis was used initially to remove populations that showed significant signs of admixture resulting from previous stocking events. Genetic stock identification (GSI), a hierarchical process for determining genetic structure across a landscape that incorporates genic differentiation, cluster analyses, and analysis of molecular variance (AMOVA), was used to delineate genetic structure. Analysis of 39 populations using GSI identified 30 unique gene pools in the dataset. Because of the limitations of managing for this many genetic units, we identified putative management units as cluster scenarios where the ratio of among-group variance (V_a) to within-group variance (V_b) was greater than one. This approach identified three groups corresponding to a Wisconsin River Genetic

Unit, upper Chippewa River Genetic Unit, and inner Chippewa River Genetic Unit. Although these units don't strictly adhere to current watershed basins, they do represent geographically cohesive groups. Both geographical (headwater capture following glacial recession) and anthropogenic (supplemental stocking) effects can logically explain the observed genetic structure. Further research should help elucidate the underlying processes responsible for the current genetic delineation.

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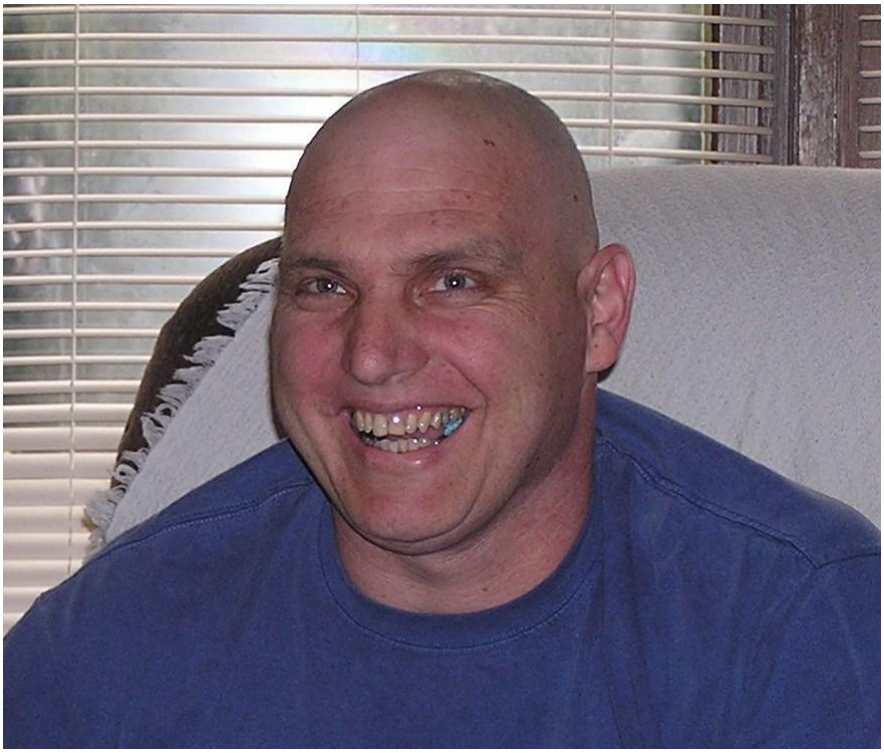

To you dad, you have been a true inspiration and the best role model a son could ask for. Thank you for always pushing me to do my best and believing in me every step of the way. You are sorely missed.

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INTRODUCTION

Artificial propagation and supplemental stocking are intended to increase fish population size. Despite the perceived benefits, artificial propagation can jeopardize the genetic integrity of native populations (Miller and Kapuscinski 2003). Busack and Currens (1995) presented four types of genetic hazards when using hatchery-raised fish: extinction, loss of within-population genetic variation, loss of between-population genetic variation, and domestication selection. The result of such actions could include drastic changes in genetic diversity (both higher and lower) and a failure to observe consistent geological and genetic relations among populations. Hindar et al. (1991) discussed the effects of hatchery raised salmonids on native populations and concluded that propagation and successful reproduction led to the breakdown of adaptive gene complexes (Whitlock et al. 1995; Orr 1996; Fenster et al. 1997; Turelli et al. 2001), thus reducing population fitness (a phenomenon known as outbreeding depression; Dobzhansky 1937; Muller 1940). Hindar et al. (1991) also determined that artificially propagated fish can decrease the population size of native fish from increased competition for breeding sites and reduced fitness of progeny through outbreeding depression. Ultimately, this reduction in population size leads to decreased genetic diversity via genetic drift and inbreeding and, subsequently, lower viability.

A species' adaptive potential is dependent upon maintaining the abundance and diversity of individual stocks. This concept, known as the stock concept (Shaklee and Currens 2003), has been a central focus of fish management for nearly 50 years (Carvalho and Hauser 1994). Delineation of specific stocks should be of foremost importance when attempting to conserve genetic integrity and effectively manage a

resource (Shaklee and Currens 2003). There are several definitions of stocks in fisheries. Ihssen et al. (1981) defined a stock as "an intraspecific group of randomly mating individuals with temporal and spatial integrity". Other definitions (e.g., Maclean and Evnas 1981, Dizon et al. 1992, and Carvalho and Hauser 1994) build on Ihssen et al. (1981) by incorporating varying degrees of temporal and spatial integrity. Regardless, separate stocks tend to demonstrate differences in some key biological/ecological attributes such as growth rate, population dynamics, habitat selection, etc. that collectively warrant designation as unique stocks (Carvalho and Hauser 1994; Van den Avyle and Hayward 1999). As such, a stock can comprise one or many populations.

To minimize the potential loss of genetic variation in natural populations, propagation programs should adhere to a strict set of guidelines aimed at protecting the genetic integrity of natural populations when choosing and spawning broodstock, and when rearing and stocking their progeny (Miller and Kapuscinski 2003). Such guidelines call for an accurate description of the contemporary genetic composition of managed stocks. Reproductively isolated subpopulations within a species maintain unique genetic diversity and, cumulatively, the adaptive potential of the entire species (Shaklee and Currens 2003). Identifying stock structure is fundamentally important when enhancement programs are implemented to: 1) accurately create an appropriate design for supplementing native stocks, 2) attempt to maintain the diversity and integrity of naturally reproducing stocks, and 3) effectively monitor and evaluate enhancement programs (Shaklee and Bentzen 1998).

Muskellunge (*Esox masquinongy*) are native to a variety of lakes and rivers throughout a restricted geographic range in North America and are suspected to have

evolved from an Esocid ancestor about 25 million years ago (Wilson 1980). The native distribution of muskellunge in North America ranges from the eastern United States in Tennessee to the upper Midwest and into portions of eastern and central Canada (Oehmcke et al. 1974; Becker 1983; Crossman 1986). Fossil records indicate that the past distribution of muskellunge was much larger than present, including portions of Oklahoma and west to Oregon (Cavender et al. 1970; Crossman 1986). During the Wisconsinan glaciations, the Mississippi refugium was likely the only overwintering place of muskellunge, thus limiting the current distribution patterns (Underhill 1986). In Wisconsin, muskellunge populations persist in over 700 lakes and 83 streams, mostly in the northern third of the state (Simonson 2008). They are thought to be native to the Chippewa River, Lake Superior, Wisconsin River, and portions of the Lake Michigan basins (Green 1935; Becker 1983)(Figure 1). Muskellunge are renowned for being top predators, often consuming large amounts of smaller prey species including various percids, catostomids, cyprinids and, occasionally, small mammals and waterfowl (Becker 1983). As top predators, muskellunge populations are naturally low with typical densities of ≤ 1.0 fish/hectare common (Simonson 2008).

The Wisconsin Department of Natural Resources (WDNR) adopted a muskellunge management plan with four main goals collectively aimed at maintaining and/or improving muskellunge fishing statewide. One of these goals was to protect the genetic integrity of self-sustained populations (Simonson 2008). Muskellunge management practices are influenced by *a priori* population designations (Table 1). Three primary muskellunge population categories exist: Category 1 waters consist of self-sustained populations that receive no supplemental stocking, Category 2 waters

exhibit natural recruitment, however, they are supplemented by stocking, and Category 3 waters don't show any known natural reproduction and are therefore maintained through supplemental stocking. Based, in part, on these categories, individual muskellunge populations are managed through a combination of bag limits, size limits, propagation, and a pervasive catch-and-release effort. The use of supplemental stocking coupled with naturally small population sizes likely increases the risk to the genetic integrity of native, naturally reproducing muskellunge populations. Two hatcheries provide fish for the vast number of water bodies throughout the northern portion of the state that are annually supplementally stocked (the Governor Tommy G. Thompson hatchery in Spooner services northwestern Wisconsin while the Art Oehmcke hatchery in Woodruff services northeastern Wisconsin, Figure 1). Therefore, it is vital that broodstock are properly managed to maintain genetic diversity (Sloss 2005). To accomplish this, it is imperative that the current genetic resource be well-documented and the structure of this underlying genetic diversity, in terms of distribution within populations, between populations, and similarities among groups of populations, be accurately delineated.

Current management of Wisconsin muskellunge is based on an assumption that genetic structure is largely concordant with watershed boundaries (Fields et al. 1997). Fields et al. (1997) used allozyme and mitochondrial DNA analyses to infer the presence of two to seven muskellunge genetic management zones (GMZs) throughout the upper Midwest with up to four GMZs located in northern Wisconsin. The Wisconsin GMZs closely adhered to watershed boundaries within the state. Although this was an important first step toward defining muskellunge GMZs in Wisconsin, there were significant limitations including relatively small sample sizes ($N \leq 30$) and a relatively small number

of populations (21) throughout a large geographic area (entire upper Midwest). Furthermore, Fields et al. (1997) used loci with relatively low genetic diversity (four allozyme loci with mean observed heterozygosity values ranging from 0.013 to 0.227 and two mtDNA loci that yielded within population nucleotide diversity ranging from 0.000 to 0.026 and among population nucleotide diversity ranging from -0.0001 to 0.0179) that provided low power for resolution (Ruzzante 1998). Therefore, conclusions from their study should be viewed as preliminary and not definitive of actual genetic structure.

Accurate, genetic-based information is crucial to effectively manage Wisconsin's muskellunge populations in a stock concept format. Development of a muskellunge genetic stock model will assist management and protect the current genetic integrity of self-sustained, native muskellunge populations. The goal of this project was to delineate the contemporary genetic structure among Wisconsin's naturally recruiting native muskellunge populations and assess current management units in their ability to conserve genetic integrity. The specific objective of this project was to delineate and compare contemporary genetic structure and current management units to determine if they were congruent.

METHODS

Experimental Design

To identify contemporary genetic structure, a series of iterative tests aimed at identifying the degree of genetic differences between two or more genetic samples were performed. This series of tests is collectively referred to as genetic stock identification (GSI; Shaklee and Currens 2003). Genetic stock identification incorporates hierarchical statistical tests where the results of one test are used as the null hypothesis for the next. Advantages of this approach include direct examination of stock structure by testing the null hypotheses of panmixia, wide ranges of applicability, and natural genetic variation provides the necessary information through putative neutral genetic markers (e.g., microsatellites; Shaklee and Bentzen 1998). Shaklee and Currens (2003) identified GSI as a crucial method when attempting to identify stock structure across spatial landscapes or time periods.

Experimentally, three primary considerations exist when conducting GSI: 1) what sites should be sampled, 2) how many populations to sample, and 3) what genetic data should be used. Because muskellunge are native to the northern third of Wisconsin, sampling was restricted to this region (Figure 2). It was initially assumed that genetic structure would be mostly congruent with current watershed boundaries (i.e., contemporary management units) so sample locales were distributed among the native northern muskellunge management units (Lake Superior, upper Chippewa River, upper Wisconsin River, and Green Bay)(Figure 2). Within these units, populations were chosen in consultation with WDNR biologists based on the following preferred criteria: 1) populations had to be naturally recruiting (i.e., preferably Category 1 populations), 2)

populations had to be putative native muskellunge populations, and 3) to minimize the potential effects of stocking, preferred populations were to have no to at most moderate supplemental stocking (i.e., no supplementation in the previous 10 years). To provide ample resolution, 40-50 populations were targeted for inclusion in this study while attempting to adequately represent each watershed (geographically and genetically) (Table 1; Figure 3). As recommended by Ruzzante (1998), a minimum of 50 randomly chosen spawning adults per population were targeted to provide statistical rigor in estimating genetic differences among populations. Several genetic marker types can be used to identify genetic structure. A central consideration for choosing molecular marker systems includes their degree of selective neutrality (i.e., unaffected by natural selection), mutation rate, and time since divergence of the species in question. Microsatellites fit the aforementioned criteria because they are considered to be selectively neutral (Brown and Epifanio 2003) and have a mutation rate considerably higher than most forms of nuclear DNA (generally about 1×10^{-5} per 100,000 cells; Lowe et al. 2004); sufficient to detect genetic structure, should it exist, among muskellunge populations that have recently diverged (< 10,000 years since divergence; Underhill 1986). The number of microsatellite loci used can vary depending on population size and divergence of the species in question, however, the 14 loci used in this study exceeds the minimum number (six) needed to determine genetic structure (Ruzzante 1998, Hedrick 1999, Kalinowski 2002, 2005).

Sample Collection

Samples were collected during the spring 2005, 2006, 2007, and 2008 spawning seasons in conjunction with WDNR fyke-net and electrofishing surveys. Samples consisted of a fin clip from the pelvic, pectoral, anal, or caudal fin stored in individually labeled tubes containing 95% non-denatured ethanol. Clipping techniques followed the Molecular Conservation Genetics Laboratory's (MCGL) standard operating procedure and was consistent with American Fisheries Society (AFS), American Society of Ichthyologists and Herpetologists (ASIH), and the American Institute of Fishery Research Biologists (AIFRB) approved guidelines for the use of fishes in research (http://www.fisheries.org/afs/publicpolicy/guidelines 2004.pdf). When available, archived samples (scales and fin spines) were substituted for fin clips if samples were less than 10 years old. When sampling individual muskellunge, total length (mm), weight (g), and sex were recorded when possible.

DNA Extraction

Genomic DNA from individual tissue samples was extracted using the Promega Wizard® Genomic DNA purification kit (Promega Corp., Madison, WI) modified for 96-well extractions with re-hydration of the DNA in 100 µl of Tris-low-EDTA buffer solution (TLE; 10mM NaCl, 0.1 mM EDTA, pH 8.0). Extracted DNA was quantified using a Nanodrop® ND-1000 spectrophotometer (Nanodrop Technologies, Wilmington, DE) and each sample was checked for quality via electrophoresis in a 1% agarose gel in the presence of ethidium bromide and visualized using UV-light. All DNA samples were

normalized to a final concentration of 20 ng/µL to attain consistent results during multi-locus genotyping.

Genotyping

A total of 14 microsatellite loci (Table 2) were used to determine genetic variation and stock structure of muskellunge populations throughout northern Wisconsin. Genotyping was done using five multiplex PCR reactions from Sloss et al. (2008) to amplify individual loci with fluorescently labeled primers for each sample (Table 3). Microsatellite variation was visualized on an ABI Prism™ 377XL automated DNA sequencer (Applied Biosystems, Inc. Foster City, CA). An in-lane standard (GeneFlo™ 625, Chimerx Inc., Milwaukee, WI) was included with all samples and Genescan® genetic analysis software (Applied Biosystems, Inc. Foster City, CA) identified individual genotypes that were subsequently entered into a master database.

Genetic Diversity

Several genetic diversity measures were estimated including allele frequencies per population, observed heterozygosity (H_O), expected heterozygosity (H_E), alleles/locus (A), allelic richness (A_r), and private allelic richness (i.e., alleles that are found exclusively in one population and can indicate restricted gene flow; Lowe 2004). Microsatellite Toolkit v3.1 (Park 2001) was used to calculate allele frequencies, H_O, H_E, and A. A potential impediment to genetic diversity measures is variation in sample size because populations that have a larger sample size are expected to have more alleles per locus (Kalinowski 2004a). Therefore, a rarefaction method was used to calculate A_r and

private allelic richness. HP-RARE v1.0 was used to calculate these measures (Leberg 2002; Kalinowski 2004b).

Genetic Stock Identification

A genetic stock identification (GSI) framework (Shaklee and Currens 2003) was followed to delineate stock boundaries for muskellunge in northern Wisconsin. The first step in GSI was to test all populations for conformance to Hardy-Weinberg equilibrium (HWE; Hardy 1908, Weinberg 1908), one of the fundamental assumptions of GSI. Hardy-Weinberg equilibrium assumes that in the absence of mutation, migration, natural selection, and genetic drift, and in the presence of infinite population size and random breeding, a population's allele frequencies will remain constant from generation to generation (Hardy 1908, Weinberg 1908). Therefore, a sample in HWE meets these model assumptions meaning the sample is representative of a single population. Alternatively, deviations from HWE can signal insufficient sampling (Allendorf and Luikart 2007) or the presence of multiple gene pools in a sample (Wahlund 1928). Hardy-Weinberg equilibrium estimates were performed with an exact Hardy-Weinberg test using a Markov Chain Monte Carlo (MCMC) method with 10,000 dememorization steps, 100 batches, and 10,000 iterations/batch (Guo and Thompson 1992; Raymond and Rousset 1995) in GENEPOP 4.0 (Rousset 2008). Sequential Bonferroni correction of alpha was performed to correct for multiple tests (Rice 1989).

A recognized problem associated with highly polymorphic microsatellite loci is that high numbers of alleles (and corresponding genotypes) can lead to significant deviations from HWE based on the cumulative effect of rare expected genotypes (Pamilo

and Varvio-Aho 1984). To correct for this problem, Hedrick (2000) suggested that rare genotypes be pooled. As such, genotypes with a frequency of < 1 % were pooled into one observed and one expected frequency value. The new observed and expected genotype values were then tested using a chi-square goodness of fit test in Microsoft Office Excel® 2007 (Microsoft Corporation 2007). A sequential Bonferroni correction was used (Rice 1989) with an initial $\alpha = 0.05$ to determine significance.

The next step in the analysis was to assess the independence of sampled loci, known as a gametic disequilibrium test (Raymond and Rousset 1995). If a locus experiences allele frequencies that are not independent of another locus, the two loci are said to be in gametic disequilibrium and one of the loci should be dropped from subsequent GSI analyses. To test for gametic disequilibrium, a Fisher's exact test and a MCMC method (described above) was performed using GENEPOP 4.0 (Rousset 2008). Sequential Bonferroni correction was used to correct for multiple tests (Rice 1989).

Admixture analysis— Admixed populations resulting from the introduction of genetically divergent fish can negatively impact the ability of GSI to resolve the correct genetic structure (Ruzzante et al. 2001). To determine if supplemental stocking, both documented and undocumented, had resulted in admixed populations, a test for admixture was performed on all sampled populations using STRUCTURE 2.2 (Pritchard et al. 2000; Randi and Lucchini 2002; Evanno et al. 2005; Lutz-Carrillo et al. 2006). STRUCTURE uses a Bayesian framework to determine the posterior probability of a previously set number of possible genetic units (K) in a given sample (Pritchard et al. 2000). The asymptotic value of the posterior probabilities is assumed to be associated with the correct K value in a given sample (Pritchard et al. 2000). Admixture analysis

was performed on all populations using a burn-in period of 50,000 repetitions and 50,000 MCMC repetitions, as recommended by Pritchard et al. (2000) with a K value set from one to five. If multiple gene pools were present in a given population, that population was either discarded from the final genetic stock model or the minority group of individuals was considered "foreign" to the gene pool and removed if the remaining population size was > 25.

Genetic stock identification based on analysis of molecular variance— Differences among sampled populations were initially tested using genic differentiation (Shaklee and Currens 2003, Raymond and Rousset 2005) that tests the null hypothesis that all sampled muskellunge populations are panmictic (i.e., from the same gene pool). Genic differentiation was estimated using Fisher's exact test to determine if allele frequency distributions are equivalent in all sampled populations using GENEPOP 4.0 (Rousset 2008) with 1,000 dememorization steps and 100 batches of 1,000 iterations each (Guo and Thompson 1992).

The next step of GSI was to predict groupings of populations based on genetic data for subsequent testing. The pairwise genetic distance among muskellunge populations was estimated using Cavalli-Sforza and Edwards (1967) chord distance (D_c) and an unrooted neighbor-joining (NJ) tree (Saitou and Nei 1987) was constructed to provide a visual representation of genetic similarities among populations. The D_c measure has been recommended for microsatellite data and has been shown to efficiently determine genetic distance in populations that have only recently diverged (Takezaki and Nei 1996), such as muskellunge (Crossman 1986). Estimates of D_c were performed using PowerMarker v3.25 (Liu and Muse 2005) with visualization of the NJ tree in TreeView

v1.6.6 (Page 1996). Observed splits in the NJ tree were used as initial hypotheses for subsequent tests of structure.

Next, significant differences among putative groupings had to be determined. Using the smallest number of groups from the NJ tree, analysis of molecular variance (AMOVA; Excoffier et al. 1992) was used to determine significance. Analysis of molecular variance is a genetic analysis framework where the total genetic variance is partitioned within populations (V_c), among populations within groups (V_b) and among groups (V_a). Similar to ANOVA, a test was performed to determine the significance of each partition. In this setting, AMOVA requires *a priori* defined groups of populations (Excoffier et al. 1992). This test is preferred because of minimal assumptions and high power for detecting genetic structure (Lowe et al. 2004). When there was significant among group variance (V_a) without significant within grouping variance (V_b), it was concluded that biological relevance was attained. Initially, populations were divided into two groups based on a combination of the NJ tree and F_{ST} values. This scenario was tested in the AMOVA framework and through several iterations the initial two group scenario was partitioned into a stable number of groups (i.e., lowest number of groupings with non-significant V_b and significant V_a). Because of the maximization of intergroup heterogeneity while maintaining low intragroup heterogeneity, groupings were determined to be putative genetic stocks. All AMOVAs were performed using Arlequin v3.11 (Excoffier et al. 2005) with 15,000 permutations and 5,000 pseudoreplicates.

The final test of GSI was to confirm stable groupings identified through AMOVA. Wright's (1931) fixation index (F_{ST}), is one of the most universal metrics of population differentiation (Lowe et al. 2004; Allendorf and Luikart 2007). The fixation

index measures the reduction of heterozygosity within a subdivided population versus the expected heterozygosity if all subpopulations performed as a single panmictic population (Hartl and Clark 1997). Pairwise F_{ST} values were used to determine divergence of populations within groups identified from AMOVA. An F_{ST} analog, theta (θ), was used for this study because it is preferred for loci with high variability, such as microsatellites (Weir and Cockerham 1984). Theta ranges from zero, meaning all populations share the same allele frequencies, to one where all populations have completely different alleles. Significance of θ is inferred from the null hypothesis that all populations are genetically similar (i.e., $\theta = 0$). Arlequin v3.11 (Excoffier et al. 2005) was used to measure pairwise population θ values and test for significant differences using 5,000 bootstrap pseudoreplicates. Groupings that maintained genetic integrity (i.e., no significant θ tests) from tests of AMOVA and θ were deemed stable.

Current genetic management units— Current management units were tested for their genetic relevance using an AMOVA framework and assuming significant between group variance would equate to biological relevance. Each current management unit was designated a putative group. Analyses were conducted in Arlequin 3.11 (Excoffier et al. 2005) using the previously identified parameters.

Bayesian genetic stock identification— After completion of the initial Shaklee and Currens (2003) GSI method, a modified GSI approach was used to verify the findings. Unlike the previous, allele frequency based method, STRUCTURE 2.2 (Pritchard et al. 2000) incorporates a Bayesian algorithm that identifies likely groupings within a dataset that conform to gametic equilibrium and Hardy-Weinberg equilibrium. Output from STRUCTURE 2.2 includes a graph of the tested number of putative groups

versus the natural log of the probability of each group being the correct number of stable units (denoted K in STRUCTURE 2.2). The natural log of the probability will increase when there is more than one gene pool present until an asymptotic value has been reached. The number of groups that represent the asymptote of the graph represent the "correct" number of stable units. It can be difficult, however, to estimate the asymptote for the most likely number of stable units. To correct for this, Evanno et al. (2005) suggested a hierarchical method of GSI where the entire dataset is originally subjected to analysis in STRUCTURE 2.2. A series of steps are then conducted that identify the largest rate of change for K (ΔK) with the smallest variance and largest probability. The iteration with the highest probability within the most likely K value is then used to determine population groupings. Individuals within each population are assigned a probability of belonging to a particular group and populations are given an overall percentage of belonging to a group based on each individual. Through this hierarchical process, the dataset is partitioned into groupings until a K value of one is attained in all subgroups. Genetic stock identification was conducted on all populations using the aforementioned approach with the modification of Coulon et al. (2008) that requires a population have 60% inclusion in a group to be considered part of that group (i.e., $\geq$ 60% of each population's genetic material assigns to a particular group). Populations that were less than 60% assigned to a group were assumed to be independent and, therefore, their own gene pool (see Figure 4 for a hypothetical scenario). An initial burn-in period of 50,000 cycles followed by 50,000 MCMC repetitions was performed. *A priori* K values ranged from 1 to 10 with 10 iterations at each K value.

A potential problem with the modified GSI approach of Coulon et al. (2008) that has not yet been addressed in the literature is possible bias associated with ΔK values > 2. In other words, as the correct K value increases, there is more variance in predictions making it less likely that a population will be at least 60% assigned to a given group. To explore the impact of this issue, a Bayesian GSI technique was performed on all populations using an absolute assignment method where populations were assigned to a group based on the highest probability regardless of the 60% threshold. Parameters in STRUCTURE 2.2 were the same as described previously.

Estimating New Genetic Management Units.

Genetic stock identification likely overestimates the number of genetic units present in populations with essentially no gene flow such as muskellunge (Waples and Gaggiotti 2006). A novel metric was used to delineate manageable genetic units of muskellunge. Genetic variance in a spatial setting, as in AMOVA, is partitioned among groups (V_a), among populations within groups (V_b), and within populations (V_c). A ratio of among group variance (V_a) to within group variance (V_b) can be used to estimate the relative proportion of overall variation accounted for among groups. Hierarchical groupings from previous analyses (GSI and STRUCTURE) were used initially to determine the V_a/V_b ratio among groups beginning with two hierarchical groups. Fixation index (θ) values were then incorporated to assign populations to particular groups until V_a/V_b exceeded one with a minimum number of groupings. Subsequently, one to two groups were added to determine the increase in this ratio. Average within and

among group F_{ST} values were also recorded to compare relatedness of populations. All analyses were performed in Arlequin 3.11 (Excoffier et al. 2005) as previously described.

RESULTS

A total of 1,768 muskellunge were collected from 43 populations over the course of this four year study (Table 1; Figure 3). Samples represented 12 counties throughout northern Wisconsin, and all five of the current management units (Figure 1). Sample sizes ranged from 21 (Lower Clam Lake; LC) to 78 (Lac Courte Oreilles; LCO) with an average of 41.6 individuals (Table 4).

Genetic Diversity

On average, the studied populations showed higher polymorphism than the populations surveyed previously with allozymes and mitochondrial DNA (mtDNA) by Fields et al. (1997). Every locus was polymorphic in all 43 populations with the exception of Ema-B120 in Seven Mile Lake (SM; Appendix 1). Allelic diversity varied considerably across all populations and loci. Observed number of alleles varied from 1 at Ema-B120 in Seven Mile Lake (SM) to 20 at Ema-D5 in Little Arbor Vitae (LAV; Appendix 1). The mean number of alleles per locus ranged from 3.50 (Potter Lake; POT) to 6.29 for Caldron Falls Flowage (CF; Table 4). Allele frequencies varied greatly across populations and loci (Appendix 1). For example, the 224 allele at locus Ema-A5 was the most common allele among all populations, however, its frequency ranged from 44.4% (Big Crooked Lake; BC) to 95.5% (POT; Appendix 1) with a standard deviation of 9.83%. Among the 43 sampled populations, observed heterozygosity ranged from 0.489 in Harris Lake (HA) to 0.616 in Lac Courte Oreilles (LCO) with an average of 0.555. Allelic richness ranged widely with the largest differences occurring between Potter Lake (POT) and Lower Clam Lake (LC) at locus Ema-D6 (4.86 and 11.37, respectively; Table 5). Wisconsin's muskellunge populations exhibited relatively low private allelic richness

across all populations. Total population values ranged from 0.00 (several populations) to 3.86 in Grindstone Lake (GR; Table 6). Individual locus values were also relatively low, ranging from 0.00 (Ema-B120 and Ema-D4) to 1.40 (Ema-A102 and Ema-D6; Table 6).

Genetic Stock Identification

Significant deviations from Hardy-Weinberg equilibrium (HWE) were initially observed in 9.97% (60/602) of comparisons with an initial α of 0.05. Following sequential Bonferroni correction, 0.83% (5/602) of comparisons departed significantly from HWE. Locus Ema-D6 constituted three of the five departures (Harris Lake, West Chippewa Flowage, and Lost Land Lake) while Ema-C1 in Plum Lake (PM) and Ema-A10 in North Nokomis Lake (NN) were the remaining two departures. When rare genotypes were pooled, only Ema-D6 in HA was significantly out of HWE proportions. Because only one locus/population comparison departed from HWE, all loci and sampled populations were considered to conform to HWE.

Out of 3,913 locus/locus comparisons per population, 301 (7.68%) initially showed signs of significant gametic disequilibrium ($\alpha = 0.05$). Following sequential Bonferroni correction, only 5 of 3,913 (0.13%) comparisons were significantly out of gametic disequilibrium. The five significant comparisons were loci Ema-A5 and Ema-D6 for Archibald Lake (AR), Ema-B110 and Ema-D114 for Harris Lake (HA), Ema-A10 and Ema-B120 for Kentuck Lake (KT), Ema-A102 and Ema-C1 for Moen Chain of Lakes (MC), and Ema-D114 and Ema-D5 for White Sand Lake (WSL). Given the small number of significant tests and lack of patterns among loci and populations, the error was assumed to be an artifact of sampling and not actual gametic disequilibrium. All

locus/population comparisons were therefore assumed to be in gametic equilibrium for subsequent analyses.

Admixture analysis— Of the 43 sampled populations, nine had no documented stocking events (Appendix 2). Since ideal populations for this study required little or no stocking, it was essential to know the potential impact of stocking on all populations. Of the 43 populations, four showed significant impacts of putative stocking events (AR, LCO, SOM, and TH; Figure 5a, b, c, and d, respectively). Bar graphs from STRUCTURE's output menu were used to identify individual admixture and either omit individuals (e.g., LCO and TH; Figure 6b and d, respectively) or omit entire populations (AR and SOM; Figure 6a and c, respectively). Bass Lake (BA) and Caldron Falls Flowage (CF) were removed from subsequent analyses because of their known history as founded populations (M.J. Jennings, Wisconsin Department of Natural Resources, personal communication), thus, violating another base requirement for inclusion in this study.

Genetic stock identification based on analysis of molecular variance— Significant genetic differences existed among sampled populations. A global test for genic differentiation produced a χ^2 value of infinity (28 degrees of freedom) with a p-value < 0.00001 meaning muskellunge populations in northern Wisconsin weren't panmictic. Locus by locus comparisons for genic differentiation were significant at all 14 loci. Of 741 pairwise population comparisons, only 23 (3.10%) were not significant, suggesting that Wisconsin's muskellunge populations do not represent a single genetic unit. Non-significant p-values (Table 7) indicated that these populations have a similar allele

frequency distribution and, therefore, gave potential *a priori* groupings to be tested in subsequent analyses.

Pairwise D_c genetic distance differed more than threefold among populations ranging from 0.0999 between Lac Courte Oreilles (LCO) and Lost Land Lake (LL) to 0.3561 between Birch Lake (BI) and Potter Lake (POT). Although resolution of internal nodes on the unrooted NJ tree was low, there was a consistent geographic split between populations from the eastern and western portions of northern Wisconsin with the exception of White Sand Lake (WSL) and Spider Lake in Iron County (SPI; Figure 7). As such, these two groupings (East vs. West) were used as initial putative groups to be tested in the AMOVA framework (

a). In doing so, significant among group (1.31% variance; $p < 0.00001$) variance and within group (3.68% variance; $p < 0.00001$) variance was detected, showing that the groups, although significant, could be structured. By iteratively breaking down putative groups through consultation with the NJ tree, D_c measures, F_{ST} values, and results from genic differentiation measurements, several hypotheses were tested and stable groupings were eventually reached. Thirty stable gene pools (among group variance $p < 0.00001$; within group variance $p = 0.06991$) were identified out of 39 populations which consisted of Group A (LC and DAY), Group B (LSG and NT), Group C (LAV and WSL), Group D (LL, TEA, LCO, and SQ), and Group E (BAV, BIG, SPI, and PM), with all other populations grouping individually (Table 8b). Following sequential Bonferroni correction of F_{ST} values, all populations within a group were not significantly different from each other (Table 9).

Current genetic management units— Initially all populations were grouped according to their current management unit for AMOVA analysis. By creating four groups consisting of the Lake Superior (AM, MN, POT, HH, HA, and PI), Green Bay (KT), upper Chippewa (BL, MCL, MOS, GR, EC, TEA, WCF, LL, WO, BC, BIG, SPI, WSL, PM, BN, LCO, LC, DAY, SS, TCF, and BI) and upper Wisconsin (NT, SQ, KA, SM, MC, SI, LSG, BAV, NN, LAV, and TH) management units, significant within and among group p-values were attained (Figure 3; Table 8c). The V_a/V_b ratio was low (0.125) suggesting that the current management units fail to represent a higher amount of genetic variation within units than among them.

Bayesian genetic stock identification— The alternative Bayesian GSI technique predicted similar but slightly different genetic structure among the sampled populations. Two groups were initially identified (approximately an east/west division) with nine populations that failed to assign to a group with ≥ 60% probability (Figure 8). Sub-group A was consistent with the western portion of Wisconsin with the exception of Squirrel Lake (SQ) and the partially assigned North and South Twin Lakes (NT; Figure 8). Group A.1 was then tested for K = 1 – 10 with two being the most likely K value, consisting of BL, MCL, MOS, and TCF (sub-group 1) and AM, DAY, LC, LCO, LL, MN, POT, and SQ (sub-group 2) with BN, EC, SS, and WCF failing to resolve in either group. Ultimately, 32 gene pools were identified consisting of AM, DAY, LC, LCO, LL, MN, POT, and SQ in one group with all other populations resolving independently (Figure 8).

Using an absolute Bayesian GSI method, hierarchical results were similar to those of the aforementioned method. All populations were initially screened for K = 1 – 10 and the most likely K value was two (Figure 9). Sub-group A, which represented the western

populations of Wisconsin with the exception of Squirrel Lake (SQ) and North and South Twin Lakes (NT), was tested for K = 1 – 10 with three being the most likely K value (Figure 9). Sixteen stable groups were identified through several iterations of the process. Final groupings included Group A.1 sub-group 1 (EC, GR, LL, NT, SQ, TEA, and WCF), Group A.1 sub-group 2 (AM, BN, DAY, LC, LCO, MN, and POT), Group A.1.3 sub-group 1 (BL, MCL, and MOS), Group B.1.1 sub-group 5 (KA, KT, and WO), Group B.1.2 sub-group 2 (BAV, BC, BIG, LSG, NN, and SI), Group B.1.2.3.2 sub-group 1 (SPI, TH, and WSL), and SS, TCF, HH, PI, HA, BI, SM, MC, LAV, and PM grouping individually (Figure 9).

Estimating New Genetic Management Units

Attempts to delineate a minimum number of genetic management units in northern Wisconsin using the novel ratio method (V_a/V_b) suggested three groups. Initially, a two group hypothesis consistent with the east/west grouping from the NJ tree (Figure 7) was tested. The V_a/V_b ratio (0.356; Table 8a) suggested these two groups were insufficient to lower genetic risk. Through several iterations (see summary, Table 10), a three group hypothesis was tested in AMOVA consisting of group 1 (Wisconsin River Genetic unit; BAV, BIG, LAV, PM, SPI, WSL, KT, NN, LSG, SI, WO, KA, MC, and BC), group 2 (upper Chippewa Genetic unit; BN, DAY, LC, LCO, LL, SQ, TEA, GR, EC, TH, WCF, AM, MN, BL, SS, and NT), and group 3 (inner Chippewa Genetic unit; MOS, MCL, and TCF). Significant differences among and within groups was attained, with a V_a/V_b ratio 1.133 (Table 8d). The average F_{ST} value within groups (0.0251) was less than half of the among group value (0.0570; Table 11). Lakes, POT, HA, HH, PI,

BI, and SM were excluded from all analyses because of their high average pairwise F_{ST} values (Table 9) and divergence observed through the above GSI methods.

DISCUSSION

Potential Admixture of Populations

Despite the initial requirement of no to limited stocking into sampled systems, several populations included in this study had been stocked extensively in the past (Appendix 2) and there were likely additional stocking events that were not documented. The impact of introgression and admixed populations on resolution of spatial genetic structure is controversial. Ruzzante et al. (2001) found that genetic stock differentiation was greater among brown trout (*Salmo trutta*) populations in Europe that received little or no stocking than populations that had been stocked for several years. In Wisconsin, stocked muskellunge appeared to have low survival to 18 months of age and even lower survival to adulthood (Margenau 1992; Margenau and Hanson 1996), suggesting that stocked individuals are not likely to contribute to the receiving population's reproduction. Franckowiak et al. (2009), however, found that walleye (*Sander vitreus*) populations in Escanaba Lake, WI (a founded population), exhibited large genetic changes over a 50-year period when supplemental stocking occurred. Of 43 sampled populations in this analysis, only nine were not stocked since 1972 (Table 1) and extensive stocking likely occurred across the landscape before then (Crossman 1986). Four populations had a high potential for admixture (Lac Courte Oreilles, Tomahawk Lake, Archibald Lake, and Somo Lake; Figure 5), indicating previous supplemental stocking events resulted in either more than one gene pool (Wahlund effect) or admixture of genetically divergent individuals. Therefore, the aforementioned admixed populations required decisions on whether or not to include them in subsequent analyses. Lac Courte Oreilles and Lake Tomahawk each had indications of two subpopulations being present. The representative

subpopulation for each system was chosen based on majority rule because it is likely that the native population would exhibit a higher sample size than stocked individuals (Margenau 1992; Margenau and Hanson 1996). A previous study (Murphy 2009) on LCO showed no significant admixture between 1956-2006, suggesting the observed admixture of the current population is a recent occurrence. Additionally, there was a high degree of differentiation (i.e., individuals had a high probability of belonging to a single group) between groups in each system suggesting that native individuals and stocked individuals do not appear to be interbreeding which supports the hypothesis of a Wahlund effect (Wahlund 1928). Archibald and Somo Lakes had a similar partition of individuals, however, the resulting sample sizes were not large enough to accurately represent their respective system in the overall analysis (Ruzzante 1998) so they were omitted.

Anomalies in the Dataset

Six populations, Birch Lake, Harris Lake, Horsehead Lake, Pine Lake, Potter Lake, and Seven Mile Lake, were not used to identify genetic management units because they exhibited high average F_{ST} values (Table 9), were highly differentiated by the neighbor-joining tree (Figure 7), and almost exclusively grouped independently of other populations through the GSI process. Interestingly, these populations occur at the outer edge of the native range of muskellunge in Wisconsin. Since the likely dispersal routes of muskellunge started at the lower reaches of the Mississippi River drainage and moved north along the Mississippi River into Wisconsin (Mandrak and Crossman 1992), it is possible that populations on the fringe suffered from a founder effect. The combination of low number of founding individuals and founding events increases the likelihood that

genetic drift quickly differentiated these populations (Hallerman 2003) resulting in the exceedingly high F_{ST} values. Consequently, it is unreasonable to use these populations when attempting to create sound genetic management units.

Other anomalies within the dataset existed in terms of the east-west geographic grouping of populations. North and South Twin Lakes and Tomahawk Lake are located in the eastern portion of the state, however, group with populations in the western portion of the state. Stocking records show North and South Twin were stocked with 500 individuals in 1986 from the Governor Tommy Thompson Hatchery in Spooner which likely had a western population broodsource (S. Gilbert, Wisconsin Department of Natural Resources, personal communication). Events like these, coupled with other potentially unknown stocking sources, could alter the genetic fingerprint of North and South Twin, explaining the grouping with western populations. Likewise, Tomahawk Lake was used as a broodsource for several years (Oehmcke 1989), and, consequently could be genetically similar to other populations because of propagation. Tomahawk Lake is also located near the border of the east/west genetic split. Katherine Lake and Squirrel Lake are also located in this region with Squirrel Lake grouping with populations in the western portion of the state and Katherine Lake grouping with populations in the eastern portion of the state (Figure 10). It is possible that these anomalies are the result of natural geological and/or biological processes. Further analysis of populations close to this region may reveal such differences.

Genetic Structure of Wisconsin's Muskellunge

Surveyed muskellunge populations in northern Wisconsin displayed unique genetic diversity consistent with life history characteristics of muskellunge and resulting in a large number of groups using GSI approaches (Table 8b; Figures 8 and 9). The high degree of structuring was consistent with other microsatellite studies of fish species. Although genetic studies involving muskellunge microsatellite DNA are lacking, a closely related species, the northern pike (*Esox lucius*), has been studied. Senanan and Kapuscinski (2000) studied northern pike populations throughout North America and Europe and found that within the Mississippi drainage all F_{ST} values were significant (mean $F_{ST} = 0.10$). Similarly, in Europe, Jacobsen et al. (2005) studied 10 northern pike populations and when partitioned into five groups for AMOVA analysis, significant within and among group variation was still observed. Other species throughout the upper Midwest that show levels of genetic structure similar to muskellunge include lake sturgeon (*Acipenser fulvescens*; Welsh et al. 2008), smallmouth bass (*Micropterus dolomieu*; Stepien et al. 2006), and walleye (Wilson and Gatt 2000).

Several factors can contribute to the level of hierarchical genetic structure observed among Wisconsin's muskellunge populations including biological, landscape connectivity, and anthropogenic forces. Life history traits of muskellunge are conducive to the high level of observed genetic differentiation. Because muskellunge often occur at low population densities (< 1 fish/acre; Simonson 2008), isolated populations will likely differentiate quickly through genetic drift and lack of migration. The relatively late maturity of muskellunge populations (3-4 years for males and 4-6 years for females; Harrison and Hadley 1979) and iteroparous life-history slow the effects of genetic drift, however, because of the increased generation time and high potential number of

spawning events per individual (Oehmcke et al. 1974; Allendorf 1983; Younk and Strand 1992; Allendorf and Luikart 2007). Nevertheless, the high pairwise divergence among virtually all populations was consistent with genetic drift strongly differentiating populations.

Geographical processes have likely minimized the effects other evolutionary forces such as migration and mutation have had on genetic diversity in Wisconsin's native muskellunge populations. Microsatellite markers have a mutation rate of ~ 1×10^{-5} per 100,000 cells (Liu 2007) so completely isolated populations will accumulate private alleles over time from chance alone. The relatively recent divergence of the studied populations (~ 10,000 years since the last glaciations; Pielou 1991) means that mutations were not likely to occur at high frequencies, consistent with the low private allelic richness observed (Table 6). The significant genetic differences observed among Wisconsin's muskellunge populations suggest genetic drift was more influential than mutation.

Migration of individuals was likely much higher during and immediately after the Wisconsonian glacial period as demonstrated by Mandrak and Crossman (1992) for other species. Moreover, recolonization at that time occurred relatively quickly as there were more water bodies and connections between them; events mediated by receding glaciers (Clayton and Moran 1982; Dyke and Prest 1987). As dispersal routes shifted and eventually disappeared, migration routes were in essence eliminated, allowing populations to differentiate from their closest neighbors. The number of observed gene pools in this study was consistent with a lack of contemporary migration routes for Wisconsin muskellunge populations.

Some muskellunge populations, especially in the extreme northern native range, likely differentiated quickly from a combination of lack of migration routes and a founder effect. A founder effect is a dramatic change in allele frequencies that occurs when a new population is established from a small number of individuals (Allendorf and Luikart 2007). Because a small number of individuals may not accurately represent the genetic diversity of the source populations, differences in allele frequencies and subsequent genetic drift (because of small population sizes) could rapidly differentiate populations in a stochastic manner. The muskellunge populations from the northern most part of the range (including Harris Lake, Horsehead Lake, Birch Lake, Pine Lake, and Mineral Lake) had, on average, lower observed heterozygosities (Table 4) than other populations, consistent with expectations if genetic drift and founder effects were strong influences on these populations' genetic diversity. The same populations also failed to group significantly with other populations in GSI analyses consistent with the stochastic nature of these two combined processes.

Anthropogenic forces may have contributed to the high degree of genetic structure observed among Wisconsin's muskellunge populations. The Governor Tommy G. Thompson Hatchery (GTH) in Spooner and Art Oehmcke Hatchery (AOH) in Woodruff (Figure 1) have served as the main hatcheries for muskellunge propagation in the western and eastern portion of Wisconsin, respectively. Brood source populations have undoubtedly varied but Lac Courte Oreilles has been used extensively at GTH while the Minocqua chain of lakes and Squirrel Lake have been commonly used at AOH (Oehmcke 1989; J. Kubisiak, Wisconsin Department of Natural Resources, personal communication). Since the early 1900's, many muskellunge populations have been

extensively stocked from these and other sources (see Appendix 2), therefore, acting to homogenize once genetically divergent populations. In essence, human movement of hatchery-raised muskellunge has artificially introduced migration. However, because of the high degree of observed variation through the identified unique gene pools and significant population pairwise F_{ST} values (Table 9), it is not likely that propagation has contributed to the observed genetic structure. Furthermore, the admixture analyses indicated that propagated individuals likely failed to significantly contribute to reproduction. Current findings are consistent with those of Margenau (1992) and Margenau and Hanson (1996) for Wisconsin muskellunge. However, the results are drastically different than the vast admixture history of Moose Lake (MN) muskellunge observed by Miller et al. (2009).

Contemporary Management Units

Current muskellunge management units are based largely on watershed boundaries that likely reflect post-glacial dispersal patterns and therefore contain genetically similar populations (Fields et al. 1997). These management units, however, failed to resolve acceptable groupings through AMOVA (significant within and among group variance and $V_a/V_b = 0.125$; Table 8c). Therefore, it is likely that continued reliance on current management units will not adequately protect the genetic integrity of individual populations. The lack of a strong watershed/genetic relationship could be the result of many factors, including stochastic changes in rates and direction of divergence among populations, previous stocking events that did not adhere to current watershed

boundaries, and/or differences between current and historic watershed boundaries in northern Wisconsin.

Small populations, such as muskellunge, are at a higher risk of random genetic effects than larger populations (Allendorf and Luikart 2007). Allendorf and Luikart (2007) stated that small populations will experience stochastic genetic change as a result of genetic drift while large populations will maintain stable allele frequencies. In northern Wisconsin, it is likely that a small number of individuals founded native water bodies via dispersal routes. Therefore, stochastic events could differentiate populations to the point that consistent genetic structure would not be identifiable. However, consistent genetic structure was identified throughout the landscape, suggesting that random events (i.e., genetic drift), although critical in the divergence of populations, has not been sufficient to eradicate the underlying genetic signal of relatedness and connectivity among populations. Therefore, the observed patterns could be correct and current watersheds are not consistent.

Stocking events also could have contributed to the observed genetic structure, especially considering that previous stocking events did not always adhere to genetic or watershed boundaries (Oehmcke 1989). If propagation caused the observed inconsistency between genetic and watershed boundaries, populations would be expected to lose genetic variation through introgression of "foreign" individuals (Hindar et al. 1991). Such phenomena would occur because the "pooling" of genetically differentiated muskellunge populations would reverse the natural forces of differentiation and homogenize unique populations. Ruzzante et al. (2001) studied brown trout populations throughout Denmark and observed lower levels of divergence among regions that were

heavily stocked compared to those that received little to no stocking. The delineation of 30 unique muskellunge gene pools through a classical GSI technique (Table 8b) and 32 through a Bayesian approach (Figure 8) along with relatively long branch lengths of the unrooted NJ tree (Figure 7) suggested that muskellunge have not been significantly impacted by propagation in northern Wisconsin. Consequently, historic geological patterns represent the most parsimonious explanation for inconsistencies between the current genetic structure of muskellunge and contemporary watershed boundaries.

Genetic Management Units

Using the novel V_a/V_b ratio, a consistent hierarchical structure suggesting three management units was resolved. These three units are the Wisconsin River Genetic unit (Big Crooked Lake, Big Arbor Vitae, Little Arbor Vitae, Big Lake, Plum Lake, Spider (Iron County) Lake, White Sand Lake, Kentuck Lake, North Nokomis Lake, Little St. Germain, Seven Island Lake, Moen Chain of Lakes, Wolf Lake, and Lake Katherine), the upper Chippewa River Genetic unit (Butternut Lake, Day Lake, Lower Clam Lake, Lac Courte Oreilles, Lost Land Lake, Squirrel Lake, Teal Lake, Lake Grindstone, East Chippewa Flowage, West Chippewa Flowage, Lake Tomahawk, Amnicon Lake, Mineral Lake, Blaisdell Lake, Spider (Sawyer County) Lake, and North and South Twin Lakes) and an inner Chippewa River Genetic unit (Moose Lake, Mud-Callahan Lake, and Tiger Cat Flowage). Initial hierarchical groupings resolved an east/west geographic split that was observed in both the classical GSI approach of Shaklee and Currens (2003; Table 8a) and the modified GSI approaches using a Bayesian method (sub-groups A and B; Figures 7 and 8). The next step in the hierarchical AMOVA process resulted in three units

(Wisconsin River, upper Chippewa, and inner Chippewa genetic units) exhibiting a ratio of 1.133 (Table 8d, Figure 10). Average F_{ST} values within the three resolved groups (mean = 0.0251) was less than half that among groups (mean = 0.0570), further showing that populations within the three genetic units were more closely related to each other than populations outside of those groups (Table 11).

The three proposed genetic units are inconsistent with current watershed boundaries. These discrepancies are consistent with geological influences, human influences, or some combination of each. Hydrological and geological events have likely contributed to the observed contemporary genetic structure. Muskellunge likely persisted solely in the Mississippian refugium and only recolonized northern Wisconsin between 9,000 and 10,000 years before present (Underhill 1984; Mandrak and Crossman 1992). Dispersal likely occurred via the Mississippi River, Wisconsin River, and Chippewa River (Underhill 1984), and, populations subsequently genetically differentiated. Although individual populations currently show unique genetic diversity signatures (i.e., significant genic differentiation observed among all populations and highly significant pairwise F_{ST} values) the degree of differentiation should be directly proportional to time since isolation (Brown and Epifanio 2003). For example, Wolf Lake and the Moen Chain of Lakes have significantly different F_{ST} values ($P < 0.00007$; Table 9) which is indicative of localized differentiation. However, when observing the entire landscape they grouped together using the novel V_a/V_b ratio (Table 8) suggesting that although these populations are genetically unique, they have a more recent time since divergence than populations outside of this group. Therefore, hierarchical structuring has been observed that supports historical hydrological patterns and geological events.

A possible explanation for the differences between genetic structure and current hydrological patterns is previous stocking events. Initial estimates of genetic structure showed a general east/west split; consistent with the locations of two hatcheries that propagate muskellunge into these areas (Art Oehmcke State Fish Hatchery in Woodruff services eastern populations and the Governor Tommy G. Thompson State Fish Hatchery in Spooner services western populations; Figure 1). However, if propagated fish have introgressed into populations, individual populations would be expected to show lower genetic diversity and reduced genetic differentiation. Allendorf and Luikart (2007) stated that repeated migration (supplemental stocking) of only a few individuals per generation will maintain similar allele frequencies among populations. Retention of high diversity within populations, coupled with hierarchical structuring consistent with landscape features suggests other factors have formed or strongly influenced the observed differences and stocking may have had a minimal role in the observed structure.

The resolution of two management units in the Chippewa River basin may be the result of aggressive impacts of stocking. The inner Chippewa River group (Moose Lake, Mud-Callahan Lake, and Tiger Cat Flowage) consists of populations that are thought to contain relatively high densities of muskellunge and are known as slow-growth/small-growth fisheries (Margenau and Hanson 1996). However, the potential exists that these populations are actually a remnant of the native Chippewa River genetic resource that resisted supplemental stocking largely because of their density and, subsequently, a competitive advantage when extraneous muskellunge were supplementally stocked into these populations (Hesthagen et al. 1999). Under this scenario, the remaining populations in the Chippewa River watershed show cohesiveness largely due to potential

introgression with hatchery fish over multiple generations of supplemental stocking. Although this scenario is a possibility, previous research indicated temporal genetic integrity of multiple fisheries despite supplemental stocking (Ruzzante et al. 2001), including muskellunge in Lac Courte Oreilles (Murphy 2009). This previous temporal stability suggests the resolution of the remaining Chippewa River populations as a single management unit would require extensive successful supplementation similar to that observed in Miller et al. (2009); a scenario that is not supported by the temporal Wisconsin muskellunge data or studies of other inland species (Jennings et al. 2005). Regardless, the inner Chippewa River management unit currently represents a cohesive biological unit that should be treated as a separate unit from the other Chippewa River populations.

Headwater capture is another possible explanation for the inconsistencies between genetic structure and hydrological boundaries in the far northern edge of the upper Chippewa River and upper Wisconsin River management units. Bishop (1995) stated that fish genetic data can be used to reveal drainage history of a landscape and several studies have shown this phenomenon. The genetic structure of the mottled sculpin (*Cottus bairdi*) in a region of Pennsylvania was determined to be strongly influenced by headwater capture (Howard and Morgan 1993). Likewise, Poissant et al. (2005) studied brook charr (*Salvelinus fontinalis*) populations in Newfoundland, Canada and found that current stream structure failed to explain genetic relationships but past hydrologic events did. The genetic data on muskellunge in this study are consistent with a hydrological pattern where the northern edge of the upper Chippewa drainage was part of the upper Wisconsin drainage when muskellunge migrated to the area following the Wisconsonian

glacial period. Five populations (Spider Lake in Iron County, Wolf Lake, Big Lake, Big Crooked Lake, and White Sand Lake; Figure 10) are located in the upper Chippewa River watershed yet genetically group with populations in the Wisconsin River watershed. Squirrel Lake and Lake Tomahawk, on the other hand, are located in the Wisconsin River watershed and group with populations in the upper Chippewa River watershed; however, extensive stocking (Appendix 2) has likely influenced these systems. These populations support the idea of headwater capture, or other geological events, where after colonization and establishment of populations, small changes in the geological landscape altered hydrologic patterns to those observed today.

Management Implications

The Wisconsin Department of Natural Resources adopted a muskellunge management plan with a specific goal of conserving the genetic integrity of self-sustained muskellunge populations. To achieve this, sound, biologically relevant management units based on contemporary genetic structure are necessary to conserve genetic diversity and maintain adaptive potential within populations. Contemporary, watershed-based, management units are inconsistent with genetic structure observed in this study. Supplementally stocking populations, even within these regions, could eventually lead to the unintentional homogenization of genetically diverse populations, therefore reducing differentiation and ultimately adaptive potential.

This study has shown there is substantial differentiation among Wisconsin's naturally recruiting muskellunge populations. Identification of 30 unique gene pools through a classical GSI technique and 32 and 16 gene pools, respectively, through two

separate Bayesian techniques indicate localized differentiation. There is a high probability that individual populations have, to some degree, independently adapted to their local water body, making adequate brood-source selection for an entire region difficult at least.

When supplemental stocking is deemed necessary to augment natural populations, the three genetic management units identified through a combination of AMOVA, V_a/V_b, STRUCTURE, and F-statistics should be sufficient to achieve economic feasibility while reducing genetic risks. Populations on the extremes of the native range of muskellunge in Wisconsin warrant special concern because of their likely founding effect identified in this study. A more in-depth analysis of these populations may be necessary to determine the potential for adverse effects such as outbreeding depression resulting from propagation. For example, Goldberg et al. (2005) found increased disease susceptibility in largemouth bass (*Micropterus salmoides*) progeny resulting from the propagation of individuals from two geographically and genetically distinct populations. Similarly, Gharrett et al. (1999) found decreased fitness in F_2 hybrids of pink salmon (*Oncorhynchus gorbuscha*) when genetically divergent populations were crossed.

Beyond the scope of strict genetic consequences, it is recognized that genetically similar populations exhibit similar biological and life history traits such as fitness and productivity (Shaklee and Currens 2003). Therefore, management for life history characteristics should follow genetic boundaries to some degree. Exceptions to these are environmental variation that may outweigh genetic similarities when determining growth rate, age at maturity, recruitment, etc. Ultimately, increased knowledge of muskellunge genetic stock structure in Wisconsin should benefit management and sustainability into

the future while minimizing potentially adverse genetic risks associated with supplementally stocking native waters.

Future Research

Additional research on current topic— Throughout the duration of this project several avenues of research have been identified that would likely help solidify and clarify some of the findings. One future research item would be to increase both the number of loci and number of populations sampled. More loci could help resolve some of the ambiguous structure observed. Increasing the number of populations sampled could strengthen management boundaries, especially if these populations occur in the regions of conflict between the hydrological patterns and genetic structure. The headwater regions of the current upper Chippewa management unit and eastern portion of the Lake Superior management unit are areas that could benefit from more sampling. Likewise, the area including Tomahawk Lake, Squirrel Lake, and Katherine Lake are likely near the genetic boundaries. Further sampling within this region could help determine fine-scale boundaries in the genetic units. Minimizing the variance in sample size by re-sampling some populations to achieve > 50 individuals in all sampled populations could also reduce some of the variance.

A study aimed at better understanding biological and population characteristics of northern Wisconsin muskellunge populations and relating these attributes to the genetic structure would be beneficial for managing muskellunge in a biologically-sound basis. Such a study could determine if Wisconsin muskellunge show biological and population dynamic differences among genetically different stocks. Characteristics such as growth rate, fecundity, recruitment, age at maturity, and length at infinity should be included in future studies such as this.

Genetic stock identification of non-propagated fish species throughout northern Wisconsin— A final future research direction that could strengthen this research is a study that looks to identify the genetic structure of non-propagated, non-sportfish populations to determine if non-game genetic structure is similar to that of muskellunge in northern Wisconsin. This study is currently being proposed using rock bass (*Ambloplites rupestris*) and log perch (*Percina caprodes*). Results from such a study could help determine if the strong hierarchical east/west split with muskellunge is consistent with zoogeography and geological processes of the region or an artifact of extensive stocking. These results could also help to identify inconsistencies in the current watershed boundaries and genetic management units where events such as headwater capture may have occurred following recolonization of northern Wisconsin. Such events have been documented in other non-sportfish populations including galaxiid fishes (*Galaxias* spp.; Burridge et al. 2006; 2007) and mottled sculpin (Howard and Morgan 1993).

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Table 1. General information on all populations included in this study. Included are abbreviations for each population, recruitment category (Class), County population occurs in, year of last recorded (WDNR) stocking, and current management unit. Asterisk denotes populations collected by Murphy (2009).

Population	Abbreviation	Class	County	Last Stocked	Management Unit
Amnicon Lake	AM*	2	Douglas	1997	Lake Superior
Archibald Lake	AR	1	Oconto	2005	Green Bay
Bass Lake	BA	1	Washburn	1984	St. Croix
Big Arbor Vitae	BAV*	2	Vilas	2004	Upper Wisconsin
Big Crooked Lake	BC*	2	Vilas	1975	Upper Chippewa
Big Lake	BIG	2	Vilas	2001	Upper Chippewa
Birch Lake	BI*	1	Vilas	1980	Upper Chippewa
Blaisdell Lake	BL	2	Sawyer	1997	Upper Chippewa
Butternut Lake	BN*	2	Price	1999	Upper Chippewa
Caldron Falls	CF*	2	Marinette	2005	Green Bay
Day Lake	DAY*	1	Ashland	1990	Upper Chippewa
East Lake Chippewa	EC*	2	Sawyer	2008	Upper Chippewa
Grindstone Lake	GR	3	Sawyer	2007	Upper Chippewa
Harris Lake	HA*	1	Vilas	1978	Lake Superior
Horsehead Lake	HH*	1	Vilas	No Record	Lake Superior
Katherine Lake	KA	1	Oneida	1999	Upper Wisconsin
Kentuck Lake	KT*	1	Nicolet/Vilas	No Record	Green Bay
Lac Courte Oreilles	LCO	3	Sawyer	2007	Upper Chippewa
Lake Tomahawk	TH*	2	Oneida	2000	Upper Wisconsin
Little Arbor Vitae	LAV	2	Vilas	2007	Upper Wisconsin
Little St. Germain	LSG	2	Vilas	2006	Upper Wisconsin
Lost Land Lake	LL	2	Sawyer	2007	Upper Chippewa
Lower Clam Lake	LC*	2	Sawyer	No Record	Upper Chippewa
Mineral Lake	MN*	1	Ashland	1976	Lake Superior
Moen Chain	MC	1	Oneida	1989	Upper Wisconsin
Moose Lake	MOS	1	Sawyer	No Record	Upper Chippewa
Mud/Callahan Lake	MCL*	1	Sawyer	1982	Upper Chippewa
N+S Twin Lake	NT*	2	Vilas	1995	Upper Wisconsin
North Nokomis Lake	NN*	2	Oneida	1996	Upper Wisconsin
Pine Lake	PI*	1	Iron	1975	Lake Superior
Plum Lake	PM	2	Vilas	1999	Upper Chippewa
Potter Lake	POT	1	Ashland	No Record	Lake Superior

Table 1. (Continued).

Lake	Abbreviation	Class	County	Last Stocked	Management Unit
Seven Island Lake	SI*	2	Lincoln	1976	Upper Wisconsin
Seven Mile Lake	SM	1	Oneida	No Record	Upper Wisconsin
Somo Lake	SOM	2	Lincoln	2007	Upper Wisconsin
Spider Lake	SPI	2	Iron	1990	Upper Chippewa
Spider Lake	SS*	1	Sawyer	1984	Upper Chippewa
Squirrel Lake	SQ	1	Oneida	2005	Upper Wisconsin
Teal Lake	TEA	2	Sawyer	2007	Upper Chippewa
Tiger Cat Flowage	TCF	1	Sawyer	No Record	Upper Chippewa
West Lake Chippewa	WCF*	2	Sawyer	2008	Upper Chippewa
White Sand	WSL	2	Vilas	No Record	Upper Chippewa
Wolf Lake	WO*	2	Vilas	No Record	Upper Chippewa

Table 2. PCR reaction recipes, fluorescent labels, and thermocycler temperature profiles for all multiplexes used (developed by Sloss et al. 2008). 10x Buffer refers to Fisher Scientific (Pittsburgh, PA) 10x PCR Buffer B without $MgCl_2$ and dNTPs refers to deoxynucleotides at equal concentration. All reactions were run in 10µL volumes with ~75 ng DNA/reaction.

Locus	Multiplex	10x Buffer (Conc.)	dNTPs (Conc.)	$MgCl_2$ (Conc.)	Primer Forward (Conc.)	Primer Reverse (Conc.)	Label
Ema-A5	1	1.00x	1.60mM	1.50mM	0.25µM	0.25µM	Ned
Ema-A10					0.20µM	0.20µM	Hex
Ema-D12a					0.10µM	0.10µM	6Fam
Ema-A102	2	1.20x	0.60mM	1.50mM	0.09µM	0.09µM	Ned
Ema-B120					0.28µM	0.28µM	Ned
Ema-D4					0.10µM	0.10µM	6Fam
Ema-A11	4	0.50x	0.60mM	1.80mM	0.10µM	0.10µM	Ned
Ema-B110					0.12µM	0.12µM	Hex
Ema-D114					0.12µM	0.12µM	6Fam
Ema-D5	3	1.20x	0.60mM	1.5mM	0.12µM	0.12µM	Hex
Ema-D6					0.20µM	0.20µM	6Fam
Ema-D116					0.15µM	0.15µM	Ned
Ema-A104	1	1.00x	0.60mM	1.50mM	0.20µM	0.20µM	6Fam
Ema-C1					0.20µM	0.20µM	Ned

1. 94°C for 2 min. 2 series of 35 cycles each at 94°C for 45 s, then 54°C annealing for 45 s. 72°C for 45 s then a final elongation of 72°C for 20 min.

2. 94°C for 2 min. 2 series of 35 cycles each at 94°C for 45 s, then 57°C annealing for 45 s. 72°C for 45 s then a final elongation of 72°C for 20 min.

3. 94°C for 2 min. 2 series of 35 cycles each at 94°C for 45 s, then 59°C annealing for 45 s. 72°C for 45 s then a final elongation of 72°C for 20 min.

4. 94°C for 2 min. 2 series of 35 cycles each at 94°C for 40 s, then 60°C annealing for 40 s. 72°C for 60 s then a final elongation of 72°C for 20 min.

Table 3. Microsatellite loci used in the current study with description of primer sequence, size range, and number of alleles (Sloss et al. 2008).

Locus	Primer Sequence (5'-3')	Allele Size (bp)	Number of Alleles
Ema-A5	F: NED™-TGGGACATTTGCCTCAAG R: CCATTGGTTCCATTTATTGC	216-230	4
Ema-A10	F: HEX™-GCCAGATGTTCCTCTTCG R: TGGTCCAGAAAGCGTTATG	154-164	6
Ema-A11	F: NED™-TACCGTCACACACAGATGC R: TGGTTCTCAAACTTTTTACACC	136-150	5
Ema-A102	F: NED™-GGAACAGGTAGTGGGCAGAG R: CTTGGTGTGGGGTTTTGTG	135-137	4
Ema-A104	F: 6FAM™-TGCAGTCTGGAACGACATC R: TGCTCACAGCAATCTCATG	161-165	4
Ema-B110	F: HEX™-TGCCCCGTATCTCTCAAC R: GGGTCTGTGTGGAAATAAATG	183-191	4
Ema-B120	F: NED™-TGTTCCTGAAAGAGTTTTGTTG R: CGAGGGAGATGGAGACTG	234-236	2
Ema-C1	F: NED™-CATTGTCTGCCTGAGGTATCT R: AAATCCAGTGTGACAGAAGTTG	205-217	4
Ema-D4	F: 6FAM™-TCCCTATCGTAAATTACACACG R: CAGAATGTGGCATTTTTAACAG	196-204	5
Ema-D5	F: 6FAM™-CCGTAGACGCACAAAAAC R: TGGTTATCTGGCATCATTG	205-289	25
Ema-D6	F: HEX™-TCACTCTCGCAATTTCTATCTG R: GGGGACAGGTAATTTGTAACTG	165-265	20
Ema-D12a	F: 6FAM™-CGTATGAACAGTAGGTTTTGTCTG R: GATAGGCACAATCCACCATC	189-225	11
Ema-D114	F: 6FAM™-TGATCCACAAACACCTGAGTAG R: CAAATCCTTCCTCAACAGATTC	270-302	9
Ema-D116	F: NED™-GCAAAAGGACACAACACTG R: CGAGCAGAGGGAAACTAAG	243-287	14

Table 4. Diversity statistics (14 loci) for all sampled populations including initial and actual number of genotypes used (N_I and N_A, respectively), expected heterozygosity (H_E) and standard deviation (H_E SD), observed heterozygosity (H_O) and standard deviation (H_O SD), mean number of alleles per locus (A) and standard deviation (A_{SD}). Full population names are in Table 1.

Population	N_I	N_A	H_E	H_E SD	H_O	H_O SD	A	A_{SD}
AM	50	50	0.5719	0.0609	0.5649	0.0188	5.86	4.24
AR	31	N/A	0.5423	0.0570	0.4977	0.0242	4.29	2.92
BA	22	N/A	0.5922	0.0531	0.5842	0.0282	5.07	3.65
BAV	50	50	0.5745	0.0633	0.5471	0.0188	5.86	4.93
BC	27	27	0.5969	0.0572	0.5873	0.0253	4.71	3.31
BI	40	40	0.4989	0.0771	0.4893	0.0211	4.93	3.32
BIG	50	49	0.5732	0.0616	0.5508	0.0191	5.57	4.29
BL	22	22	0.5354	0.0624	0.5073	0.0292	4.79	3.51
BN	42	42	0.5668	0.0596	0.5476	0.0211	5.36	4.29
CF	47	N/A	0.5827	0.0611	0.6038	0.0191	6.29	5.04
DAY	50	50	0.5567	0.0612	0.5471	0.0188	5.64	3.99
EC	48	48	0.5787	0.0597	0.5797	0.0191	6.21	4.89
GR	35	35	0.6092	0.0535	0.5920	0.0223	5.79	3.91
HA	36	36	0.5366	0.0659	0.4887	0.0224	4.71	3.93
HH	23	23	0.5353	0.0582	0.5589	0.0277	4.21	2.22
KA	33	33	0.5372	0.0634	0.5365	0.0234	5.00	3.94
KT	41	41	0.5517	0.0677	0.5363	0.0208	5.21	4.08
LAV	58	58	0.5786	0.0620	0.5872	0.0177	5.71	4.98
LC	21	21	0.5725	0.0594	0.5578	0.0290	5.07	3.54
LCO	78	56	0.5854	0.0562	0.6157	0.0175	5.86	4.57
LL	57	57	0.5918	0.0573	0.5740	0.0176	6.14	4.80
LSG	48	48	0.5952	0.0563	0.5799	0.0194	6.07	4.73
MC	59	59	0.5828	0.0505	0.5967	0.0174	5.79	3.68
MCL	49	49	0.5357	0.0637	0.5266	0.0192	5.79	4.04
MN	50	50	0.5337	0.0600	0.5447	0.0189	5.07	3.93
MOS	47	47	0.5224	0.0738	0.5292	0.0196	5.00	3.44
NN	45	45	0.5516	0.0517	0.5657	0.0200	5.00	3.57
NT	34	34	0.5742	0.0532	0.5905	0.0226	5.50	4.29
PI	31	41	0.4831	0.0678	0.4927	0.0241	3.86	2.44
PM	46	46	0.5840	0.0593	0.5806	0.0195	5.79	4.35
POT	22	22	0.5029	0.0554	0.4910	0.0286	3.50	2.31
SI	46	46	0.5542	0.0661	0.5918	0.0194	4.79	3.56
SM	31	31	0.4959	0.0747	0.5076	0.0243	3.79	2.29
SOM	44	N/A	0.5735	0.0637	0.5816	0.0203	5.79	4.96
SPI	25	25	0.5607	0.0669	0.5645	0.0267	5.14	3.80

Table 4. (Continued).

Population	N_I	N_A	H_E	H_E SD	H_O	H_O SD	A	A SD
SQ	39	39	0.5579	0.0598	0.5637	0.0214	5.50	4.38
SS	39	39	0.5258	0.0711	0.5309	0.0215	5.57	4.55
TCF	46	46	0.5236	0.0638	0.5241	0.0197	5.14	3.76
TEA	48	48	0.5797	0.0608	0.5589	0.0192	5.93	4.27
TH	49	33	0.5671	0.0641	0.5715	0.0189	5.57	4.15
WCF	40	40	0.587	0.0595	0.5902	0.0209	5.57	4.27
WO	50	50	0.5367	0.0627	0.5504	0.0189	5.07	4.08
WSL	41	41	0.5953	0.0562	0.5993	0.0205	5.86	4.35
Mean	41.6	41.5	0.558	0.0614	0.555	0.0214	5.29	3.94

Table 5. Rarefacted allelic richness estimates based on the smallest sample size (N = 21; Lower Clam Lake) and associated mean values for both samples and loci (italics). Full population names are in Table 1.

	Ema-A5	Ema-A10	Ema-D12a	Ema-A102	Ema-B120	Ema-A11	Ema-B110	Ema-D114	Ema-D5	Ema-D6	Ema-D116	Ema-D4	Ema-A104	Ema-C1	*Mean*
AM	2.36	3.08	6.23	2.00	2.00	2.59	3.00	5.51	13.67	9.67	8.53	3.00	3.36	2.89	4.85
BAV	2.96	2.72	7.25	2.00	2.00	2.00	2.99	5.53	13.56	8.14	9.41	3.00	3.59	2.84	4.86
BC	3.00	2.00	5.66	2.00	2.00	2.00	3.00	4.56	10.72	8.12	9.51	3.00	3.67	2.98	4.44
BI	3.00	2.15	5.85	2.00	1.70	2.29	3.00	5.90	11.16	8.76	7.47	3.00	3.00	3.63	4.49
BIG	2.99	2.73	6.27	2.00	2.00	2.00	3.00	6.59	12.50	7.96	9.88	3.00	3.00	3.26	4.80
BL	2.00	3.71	7.89	2.00	2.00	2.00	3.00	5.78	13.38	6.00	8.58	2.97	3.00	2.97	4.66
BN	2.00	2.95	6.75	2.00	2.00	3.72	3.00	3.95	13.36	9.00	8.92	3.00	3.35	3.00	4.79
DAY	2.74	2.83	6.82	2.00	2.00	2.66	3.00	5.16	11.03	8.76	9.76	3.00	3.53	3.48	4.77
EC	2.85	2.36	7.05	2.00	2.00	3.75	3.00	5.65	14.42	10.28	9.44	3.00	3.38	3.58	5.20
GR	3.00	3.28	8.20	3.03	2.00	2.51	3.51	6.05	13.66	7.35	8.45	3.00	3.00	3.55	5.04
HA	2.77	1.94	5.84	2.00	2.00	2.00	3.00	4.75	11.68	8.83	6.67	2.94	2.99	1.94	4.24
HH	2.78	2.57	6.73	2.00	2.00	2.00	2.96	4.77	8.75	6.56	5.78	2.78	2.99	3.77	4.03
KA	2.98	1.98	6.61	2.00	2.00	2.80	3.00	4.64	13.06	6.67	7.49	3.00	3.00	2.83	4.43
KT	2.69	2.44	7.39	2.00	2.00	2.39	3.00	4.35	13.33	7.38	8.97	3.00	3.00	3.00	4.64
LAV	2.99	2.29	6.72	2.00	2.00	2.57	3.00	4.92	13.50	7.63	8.43	3.00	3.32	2.93	4.66
LC	2.00	3.86	6.84	2.00	2.00	2.86	3.00	4.98	11.42	11.37	8.93	3.00	3.00	3.86	4.94
LCO	2.79	2.69	7.08	2.00	2.00	2.86	3.00	5.18	12.60	7.91	9.79	3.00	3.69	3.24	4.85
LL	2.94	2.68	6.99	2.00	2.00	3.54	3.00	5.66	14.60	8.47	11.05	3.00	3.49	4.08	5.25
LSG	2.95	2.37	7.74	2.00	2.00	3.00	2.99	5.84	14.00	7.82	9.45	3.00	3.00	4.15	5.02
MC	2.98	3.92	6.66	3.69	2.00	3.27	2.54	4.11	11.34	6.72	8.94	3.00	4.10	3.82	4.79
MCL	2.37	2.75	6.21	2.00	2.00	3.09	2.98	6.45	11.50	8.76	7.59	3.00	3.36	3.50	4.68
MN	2.35	2.98	5.34	2.00	2.00	2.00	2.94	4.50	11.77	7.46	7.97	3.00	3.79	2.10	4.30
MOS	2.39	2.78	5.39	2.00	1.98	2.15	3.00	5.71	11.01	6.91	8.87	3.00	2.97	3.92	4.43
NN	2.96	3.24	5.86	2.00	2.00	2.99	3.00	5.68	12.12	7.00	6.85	3.00	3.00	2.79	4.46
NT	2.98	3.43	5.53	2.00	2.00	3.68	2.98	4.31	13.67	7.77	9.54	3.00	3.00	3.43	4.81
PI	3.00	1.93	4.49	1.93	2.00	2.00	2.98	3.98	8.94	7.40	4.89	3.00	3.00	1.99	3.68
PM	2.99	2.39	8.23	2.00	2.00	2.78	2.99	5.58	13.16	8.19	10.09	3.00	3.63	3.57	5.04
POT	1.97	3.00	5.64	2.00	2.00	2.00	2.00	2.00	9.77	4.86	4.98	3.00	3.00	2.00	3.44

Table 5. (Continued).

	Ema-A5	Ema-A10	Ema-D12a	Ema-A102	Ema-B120	Ema-A11	Ema-B110	Ema-D114	Ema-D5	Ema-D6	Ema-D116	Ema-D4	Ema-A104	Ema-C1	*Mean*
SI	2.88	3.26	6.92	2.00	2.00	2.00	2.98	4.76	11.99	6.25	6.17	3.00	3.00	2.65	4.27
SM	2.99	2.00	5.50	2.92	1.00	2.00	2.00	4.84	8.42	6.87	4.97	3.00	3.00	1.60	3.65
SPI	2.99	2.88	8.43	2.00	2.00	2.75	3.00	5.63	13.93	7.62	8.23	3.00	3.00	2.93	4.88
SQ	2.86	2.47	7.97	2.00	2.00	2.71	2.99	4.42	12.51	7.20	10.12	3.00	3.00	3.45	4.76
SS	2.00	2.71	5.59	2.00	2.00	2.38	2.84	6.23	13.69	9.07	10.53	2.85	3.84	2.86	4.90
TCF	2.63	2.75	5.80	2.00	2.00	3.77	2.87	4.63	12.54	8.10	6.78	2.98	2.84	2.78	4.46
TEA	3.36	2.74	6.14	2.00	2.00	3.32	3.00	6.42	13.56	7.97	9.45	3.00	3.61	3.14	4.98
TH	3.00	2.90	4.98	2.55	2.00	3.59	3.00	5.69	12.56	9.74	9.24	3.00	3.00	2.71	4.85
WCF	2.96	2.70	6.20	2.00	2.00	2.84	3.00	5.02	13.82	7.75	10.00	3.00	3.00	4.27	4.90
WO	2.75	2.69	6.53	2.00	2.00	3.73	2.90	3.72	13.80	5.18	8.51	3.00	3.00	3.00	4.49
WSL	3.60	2.88	7.64	2.00	2.00	2.44	2.99	5.54	14.26	6.68	9.91	3.00	3.44	3.87	5.02
Mean	2.76	2.75	6.54	2.11	1.97	2.69	2.93	5.10	12.43	7.80	8.47	2.99	3.23	3.14	

Table 6. Private allelic richness based on rarefaction (Kalinowski 2004b) with total values for sampled populations and individual loci (italics). Sample size was based on the smallest sample (N = 21; Lower Clam Lake). Full population names are in Table 1.

	Ema-A5	Ema-A10	Ema-D12a	Ema-A102	Ema-B120	Ema-A11	Ema-B110	Ema-D114	Ema-D5	Ema-D6	Ema-D116	Ema-D4	Ema-A104	Ema-C1	*Total*
AM	0.00	0.00	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.29
BAV	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BI	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.27	0.00	0.00	0.00	0.00	0.40
BIG	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.37
BL	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BN	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.09
DAY	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
EC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GR	0.00	0.77	0.00	0.76	0.00	0.00	0.51	0.51	0.00	0.53	0.00	0.00	0.00	0.77	3.86
HA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
HH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
KA	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08
KT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.44
LAV	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.13
LCO	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LL	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.17	0.00	0.00	0.06	0.24
LSG	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.25
MC	0.00	0.00	0.00	0.57	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.32	0.00	1.03
MCL	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MN	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.13
MOS	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NN	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
PI	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
PM	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
POT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table 6. (Continued).

	Ema-A5	Ema-A10	Ema-D12a	Ema-A102	Ema-B120	Ema-A11	Ema-B110	Ema-D114	Ema-D5	Ema-D6	Ema-D116	Ema-D4	Ema-A104	Ema-C1	*Total*
SI	0.00	0.00	0.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.37
SM	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07
SPI	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
SQ	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
SS	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.73	0.00	0.32	0.00	0.00	0.00	1.05
TCF	0.00	0.00	0.00	0.00	0.00	0.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.39
TEA	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.00	0.00	0.00	0.00	0.00	0.23
TH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01
WCF	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.12
WO	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
WSL	0.57	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.01
Total	0.60	1.14	1.30	1.40	0.00	0.56	0.51	0.52	1.15	1.40	0.49	0.00	0.45	1.12	

Table 7. Non-significant pairwise comparisons (following sequential Bonferroni correction) for genic differentiation with associated χ^2 and p-values. Full population names are in Table 1.

Pairwise Comparison	χ^2	p-value
BAV/BIG	25.245	0.6145
BAV/LAV	35.185	0.1645
DAY/LC	40.021	0.0658
LCO/LL	31.347	0.3019
BAV/LSG	32.481	0.2554
LCO/NT	40.652	0.0578
BAV/PM	27.317	0.5010
LAV/PM	38.076	0.0970
LL/PM	40.039	0.0656
LSG/PM	28.775	0.4240
NT/PM	38.542	0.0886
EC/SPI	34.263	0.1923
NT/SPI	36.683	0.1260
PM/SPI	34.252	0.1927
LL/SQ	35.188	0.1645
PM/SQ	35.650	0.1517
SPI/SQ	40.000	0.0661
LL/TEA	34.505	0.1847
PM/TEA	38.653	0.0867
SPI/TEA	40.736	0.0568
NT/TH	41.015	0.0535
TEA/TH	36.121	0.1395
PM/WSL	40.586	0.0586

Table 8. Analysis of molecular variance (AMOVA) groupings, sum of squares, percent of variation, p-values, and V_a/V_b ratio. Full population names are in Table 1.

a) 2 Group AMOVA		Source of Variation	Sum of Squares	% of Variation	p-value	V_a/V_b
Group 1	BN, DAY, LC, LCO, LL, SQ, SS, MCL, TEA, AM, MN, TCF, GR, WCF, BL, MOS, EC, TH, POT, WSL, SPI	Among Groups (V_a)	101.039	1.31	< 0.00001	0.356
		Among Populations within Groups (V_b)	588.735	3.68	< 0.00001	
		Within Populations (V_c)	12078.692	94.99	< 0.00001	
Group 2	NT, BAV, BIG, WO, LAV, PM, BC, KT, NN, HA, LSG, SM, HH, PI, KA, BI, SI, MC					

Table 8. (Continued).

b)

Genetic Stock Structure		Source of Variation	Sum of Squares	% of Variation	p-value	V_a/V_b
Group 1	LC, DAY	Among Groups (V_a)	649.678	4.30	0.06991	22.631
Group 2	LSG, NT	Among Populations within Groups (V_b)	40.097	0.19	< 0.00001	
Group 3	LAV, WSL	Within Populations (V_c)	12078.692	95.52	< 0.00001	
Group 4	LL, TEA, LCO, SQ					
Group 5	BAV, BIG, SPI, PM					
Groups 6 - 30 (all individual populations/ group)	AM, BL, BN, EC, GR, MCL, MN, MOS, POT, SS, TCF, TH, WCF, HA, HH, NN, PI, KA, SI, SM, KT, BC, BI, WO, MC					

Table 8. (Continued).

c) Current Management Units		Source of Variation	Sum of Squares	% of Variation	p-value	V_a/V_b
Group 1 (LS)	AM, MN, POT, HH, HA, PI	Among Groups (V_a)	90.838	0.51	0.01171	0.125
		Among Populations within Groups (V_b)	598.937	4.08	< 0.00001	
Group 2 (GB)	KT					
		Within Populations (V_c)	6184.000	96.53	< 0.00001	
Group 3 (UC)	BL, MCL, MOS, GR, EC, TEA, WCF, LL, WO, BC, BIG, SPI, WSL, PM, BN, LCO, LC, DAY, SS, TCF, BI					
Group 4 (UW)	NT, SQ, KA, SM, MC, SI, LSG, BAV, NN, LAV, TH					

Table 8. (Continued).

d)

Genetic Management Units		Source of Variation	Sum of Squares	% of Variation	p-value	V_a/V_b
Group 1	BAV, BIG, LAV, PM, SPI, WSL, KT, NN, LSG, SI, WO, KA, MC, BC	Among Groups (V_a)	169.845	2.21	< 0.00001	1.133
		Among Populations within Groups (V_b)	317.194	1.95	< 0.00001	
Group 2	BN, DAY, LC, LCO, LL, SQ, TEA, GR, EC, TH, WCF, AM, MN, BL, SS, NT	Within Populations (V_c)	10829.801	95.84	< 0.00001	
Group 3	MOS, MCL, TCF					

Table 9. Population pairwise F_{ST} values from Arlequin 3.11 (below diagonal) and sequential Bonferroni corrected significance values (above diagonal). Mean F_{ST} values are included in last row of matrix. Adjusted p-value = 0.00007. Full population names are in Table 1.

	AM	BAV	BC	BI	BIG	BL	BN	DAY	EC	GR	HA	HH	KA
AM	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.00034	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BAV	0.02640	-	<0.00007	<0.00007	0.8168	<0.00007	0.00047	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BC	0.05730	0.02790	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BI	0.11790	0.06940	0.07580	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BIG	0.03240	0.00120	0.03240	0.06070	-	<0.00007	0.00067	<0.00007	<0.00007	0.00088	<0.00007	<0.00007	<0.00007
BL	0.04160	0.06150	0.08140	0.12470	0.07040	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BN	0.01640	0.01390	0.05750	0.09820	0.02400	0.04230	-	0.00466	0.00027	0.00175	<0.00007	<0.00007	<0.00007
DAY	0.01200	0.01660	0.05940	0.10400	0.02400	0.04680	0.01080	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
EC	0.01770	0.01070	0.03820	0.06360	0.01430	0.02450	0.00910	0.01420	-	<0.00007	<0.00007	<0.00007	<0.00007
GR	0.01010	0.01400	0.03500	0.09230	0.01350	0.04210	0.01030	0.01690	0.01000	-	<0.00007	<0.00007	<0.00007
HA	0.06350	0.04200	0.05810	0.07960	0.05000	0.09040	0.07130	0.06270	0.04820	0.05610	-	<0.00007	<0.00007
HH	0.10420	0.07310	0.06260	0.11310	0.07240	0.11210	0.11070	0.09770	0.07750	0.08610	0.07660	-	<0.00007
KA	0.03750	0.02200	0.03870	0.06520	0.01250	0.06400	0.04260	0.03690	0.01410	0.02950	0.06200	0.09020	-
KT	0.07340	0.02730	0.04000	0.06560	0.02300	0.09330	0.06400	0.05830	0.03840	0.04560	0.04940	0.06460	0.03700
LAV	0.02440	0.00210	0.03200	0.07800	0.00850	0.06060	0.02530	0.01710	0.01570	0.01520	0.03930	0.06780	0.02420
LC	0.00310	0.01360	0.06230	0.10620	0.02080	0.05360	0.01060	-0.00040	0.01560	0.01740	0.07060	0.09820	0.03680
LCO	0.01070	0.01040	0.04800	0.08710	0.01230	0.03810	0.01090	0.00550	0.00730	0.00850	0.05760	0.08360	0.02790
LL	0.01240	0.00480	0.03810	0.08220	0.01350	0.03680	0.00800	0.00420	0.00590	0.00530	0.04290	0.07670	0.02750
LSG	0.01990	0.00070	0.02550	0.07250	0.00490	0.04270	0.02030	0.01640	0.00870	0.01200	0.04430	0.06140	0.01520
MC	0.04790	0.02760	0.04610	0.09490	0.02820	0.08880	0.04310	0.05620	0.03430	0.03320	0.06800	0.07990	0.03230
MCL	0.06920	0.06000	0.08450	0.07610	0.06100	0.06910	0.04880	0.06700	0.03480	0.06470	0.07530	0.10910	0.05730
MN	0.02950	0.03490	0.08730	0.11850	0.03310	0.06940	0.02940	0.03560	0.03730	0.03100	0.07780	0.10870	0.05010
MOS	0.07610	0.05490	0.08790	0.06780	0.05390	0.07330	0.05630	0.07050	0.03940	0.07090	0.08710	0.11610	0.05530
NN	0.06360	0.02810	0.06570	0.10660	0.02530	0.11200	0.06120	0.04200	0.04960	0.05360	0.07170	0.09500	0.04380
NT	0.01140	0.00790	0.04050	0.07890	0.00860	0.04580	0.00650	0.01490	0.00160	0.00610	0.06210	0.08730	0.01410
PI	0.12010	0.06180	0.06060	0.10610	0.07270	0.14460	0.10590	0.10230	0.07960	0.09360	0.09590	0.07690	0.08100
PM	0.02430	0.00040	0.02510	0.06320	0.00270	0.05120	0.02070	0.01380	0.00580	0.00940	0.04670	0.05870	0.01300

Table 9. (Continued).

	KT	LAV	LC	LCO	LL	LSG	MC	MCL	MN	MOS	NN	NT	PI
POT	0.06680	0.06580	0.10510	0.17040	0.09160	0.08770	0.04880	0.07110	0.06030	0.06980	0.12810	0.16640	0.09600
SI	0.05630	0.01310	0.04980	0.08380	0.01120	0.10100	0.05110	0.05490	0.03850	0.03260	0.04730	0.08930	0.03220
SM	0.10650	0.05380	0.09490	0.10180	0.05840	0.13420	0.08490	0.11580	0.07070	0.08320	0.08620	0.14520	0.06780
SPI	0.02870	0.00170	0.03360	0.05340	0.00460	0.05510	0.01870	0.01780	0.00110	0.01760	0.03080	0.06600	0.01110
SQ	0.01250	0.00830	0.03700	0.08770	0.01790	0.04040	0.01390	0.00680	0.00600	0.00760	0.05200	0.07970	0.02900
SS	0.03650	0.05180	0.08810	0.12560	0.06640	0.05350	0.03160	0.04740	0.03830	0.05030	0.09500	0.13020	0.08130
TCF	0.07210	0.06430	0.10040	0.10450	0.07440	0.07880	0.05810	0.07900	0.04320	0.06670	0.08190	0.12450	0.07360
AM	<0.00007	<0.00007	0.0608	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.0002	<0.00007
BAV	<0.00007	0.33704	<0.00007	0.0002	0.03036	0.31086	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.04852	<0.00007
BC	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BI	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BIG	<0.00007	0.00142	<0.00007	<0.00007	0.00034	0.01511	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.01012	<0.00007
BL	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BN	<0.00007	<0.00007	0.00121	0.00108	0.0168	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.02146	<0.00007
DAY	<0.00007	<0.00007	0.02564	0.00013	0.00013	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
EC	<0.00007	<0.00007	0.00034	0.0004	0.00101	0.00013	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.00628	<0.00007
GR	<0.00007	<0.00007	0.00013	0.00013	0.00094	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.00999	<0.00007
HA	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
HH	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
KA	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.00013	<0.00007
KT	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
LAV	0.01950	-	<0.00007	<0.00007	0.00013	0.00277	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.0249	<0.00007
LC	0.05660	0.01540	-	0.00169	0.00128	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.00297	<0.00007
LCO	0.04090	0.01180	0.00250	-	0.22456	0.00013	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.07476	<0.00007
LL	0.03810	0.00940	0.00730	-0.00050	-	0.00999	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.13414	<0.00007
LSG	0.02810	0.00360	0.00980	0.00400	0.00500	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.21559	<0.00007
MC	0.04780	0.03510	0.04940	0.04870	0.04030	0.03920	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
MCL	0.07190	0.06900	0.05890	0.05190	0.05400	0.05580	0.06600	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
MN	0.08150	0.04010	0.02890	0.02360	0.02640	0.03200	0.06320	0.09530	-	<0.00007	<0.00007	<0.00007	<0.00007
MOS	0.06200	0.06620	0.05950	0.05720	0.05700	0.05240	0.05960	0.02200	0.10260	-	<0.00007	<0.00007	<0.00007
NN	0.03810	0.02070	0.04030	0.04090	0.04100	0.02970	0.05930	0.11660	0.05720	0.10280	-	<0.00007	<0.00007
NT	0.04350	0.01250	0.00750	0.00340	0.00600	0.00280	0.02900	0.04280	0.02120	0.05010	0.04790	-	<0.00007

Table 9. (Continued).

	PM	POT	SI	SM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
PI	0.06350	0.06600	0.11240	0.09730	0.08200	0.07440	0.08410	0.14090	0.12910	0.13220	0.08790	0.10270	-
PM	0.02320	0.00330	0.01610	0.00520	0.00350	0.00070	0.03370	0.06020	0.02810	0.06170	0.02740	0.00630	0.05460
POT	0.12980	0.08890	0.06710	0.06190	0.05290	0.07580	0.08550	0.10120	0.05990	0.12560	0.12350	0.05540	0.17790
SI	0.02690	0.02060	0.05010	0.04070	0.04010	0.02130	0.03180	0.08680	0.05650	0.07430	0.03140	0.03410	0.08040
SM	0.06500	0.06680	0.10680	0.09020	0.08580	0.06900	0.05270	0.10320	0.09910	0.08450	0.08510	0.07400	0.10840
SPI	0.02000	0.01020	0.01960	0.01190	0.00880	0.00860	0.02420	0.03540	0.03900	0.04240	0.03610	0.00600	0.06250
SQ	0.03860	0.01280	0.00890	0.00470	-0.00090	0.01170	0.04080	0.06310	0.03020	0.06870	0.04580	0.00740	0.07770
SS	0.09460	0.05780	0.03320	0.03780	0.04020	0.04330	0.08250	0.04220	0.07830	0.05660	0.12450	0.03180	0.16850
TCF	0.08840	0.08310	0.06570	0.06280	0.05890	0.06330	0.07310	0.02530	0.09500	0.04940	0.12760	0.05310	0.14720
AM	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.00013	<0.00007	<0.00007	<0.00007
BAV	0.33623	<0.00007	<0.00007	<0.00007	0.0442	0.01309	<0.00007	<0.00007	0.00891	0.0336	<0.00007	<0.00007	0.02537
BC	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BI	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BIG	0.00614	<0.00007	<0.00007	<0.00007	0.00999	<0.00007	<0.00007	<0.00007	0.00027	0.04953	<0.00007	<0.00007	<0.00007
BL	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
BN	<0.00007	<0.00007	<0.00007	<0.00007	0.00479	0.00061	<0.00007	<0.00007	0.00452	0.00088	0.00027	<0.00007	0.0002
DAY	<0.00007	<0.00007	<0.00007	<0.00007	0.00054	0.00088	<0.00007	<0.00007	0.00034	<0.00007	<0.00007	<0.00007	<0.00007
EC	<0.00007	<0.00007	<0.00007	<0.00007	0.09217	0.0004	<0.00007	<0.00007	0.00034	0.0004	<0.00007	<0.00007	0.00013
GR	0.00661	<0.00007	<0.00007	<0.00007	0.00897	0.0581	<0.00007	<0.00007	0.00094	0.01086	0.00067	<0.00007	0.01316
HA	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
HH	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
KA	<0.00007	<0.00007	<0.00007	<0.00007	0.00027	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.0002
KT	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	0.0002
LAV	0.09318	<0.00007	<0.00007	<0.00007	0.00385	0.00013	<0.00007	<0.00007	0.00027	0.00034	<0.00007	<0.00007	0.00412
LC	0.00027	<0.00007	<0.00007	<0.00007	0.00297	0.00155	<0.00007	<0.00007	0.00027	0.00115	<0.00007	<0.00007	0.00013
LCO	0.00243	<0.00007	<0.00007	<0.00007	0.05344	0.00142	<0.00007	<0.00007	0.00472	0.00074	<0.00007	<0.00007	0.00054
LL	0.16444	<0.00007	<0.00007	<0.00007	0.08394	0.09845	<0.00007	<0.00007	0.13543	0.00499	0.00088	<0.00007	0.0135
LSG	0.12922	<0.00007	<0.00007	<0.00007	0.0253	0.00067	<0.00007	<0.00007	0.00027	0.00196	<0.00007	<0.00007	0.00169
MC	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
MCL	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
MN	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
MOS	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007

Table 9. (Continued).

	AM	BAV	BC	BI	BIG	BL	BN	DAY	EC	GR	HA	HH	KA
TEA	0.01050	0.00380	0.03950	0.08070	0.00780	0.03640	0.01050	0.00810	0.00580	0.00890	0.04150	0.07710	0.02050
TH	0.01340	0.00590	0.03180	0.07610	0.00630	0.05900	0.01340	0.01170	0.01160	0.00850	0.04470	0.08570	0.02130
WCF	0.02020	0.01090	0.03690	0.07410	0.01420	0.03330	0.01100	0.01380	0.00420	0.01120	0.05230	0.08820	0.02080
WO	0.06920	0.02290	0.04490	0.06440	0.02110	0.09350	0.05980	0.06410	0.02930	0.04940	0.06400	0.06820	0.02870
WSL	0.02410	0.00390	0.02230	0.07690	0.01290	0.04180	0.02170	0.01750	0.01130	0.01060	0.04250	0.06530	0.02280
Mean	0.04315	0.02683	0.05401	0.08862	0.03061	0.06831	0.03794	0.03983	0.02727	0.03418	0.06357	0.09069	0.04042

	KT	LAV	LC	LCO	LL	LSG	MC	MCL	MN	MOS	NN	NT	PI
TEA	0.03900	0.00310	0.00810	0.00310	0.00140	0.00530	0.03180	0.05820	0.01730	0.05890	0.02750	0.00570	0.08060
TH	0.04760	0.00750	0.01000	0.01070	0.01150	0.00640	0.03660	0.06090	0.03710	0.06360	0.03160	0.00870	0.07830
WCF	0.04030	0.01550	0.01490	0.00620	0.00850	0.00720	0.04090	0.04240	0.04300	0.04610	0.04590	0.00940	0.08480
WO	0.02710	0.03430	0.05910	0.03950	0.04160	0.02400	0.04220	0.07380	0.07000	0.06580	0.05370	0.03090	0.05350
WSL	0.01450	0.00380	0.01670	0.00910	0.00520	0.00490	0.02990	0.06120	0.04210	0.05660	0.03120	0.01450	0.06580
Mean	0.05069	0.03124	0.03772	0.03088	0.02847	0.02692	0.05021	0.06673	0.05630	0.06809	0.06031	0.02875	0.09510

	PM	POT	SI	SM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
NN	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
NT	0.08387	<0.00007	<0.00007	<0.00007	0.24676	0.10621	<0.00007	<0.00007	0.02564	0.08327	0.00081	<0.00007	0.0025
PI	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
PM	-	<0.00007	<0.00007	<0.00007	0.21552	0.06329	<0.00007	<0.00007	0.04197	0.01046	0.00013	<0.00007	0.04184
POT	0.07270	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
SI	0.02230	0.11400	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
SM	0.06910	0.14070	0.03340	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
SPI	0.00040	0.06480	0.01820	0.05450	-	0.12686	<0.00007	<0.00007	0.06505	0.02159	0.05425	<0.00007	0.04622
SQ	0.00390	0.05560	0.04420	0.09130	0.00780	-	<0.00007	<0.00007	0.00715	<0.00007	<0.00007	<0.00007	0.01592
SS	0.05820	0.09230	0.09860	0.13250	0.05740	0.04950	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
TCF	0.06880	0.09170	0.08160	0.09110	0.04290	0.06440	0.05170	-	<0.00007	<0.00007	<0.00007	<0.00007	<0.00007
TEA	0.00210	0.06010	0.02830	0.06890	0.00610	0.00390	0.04800	0.06850	-	0.1166	0.00013	<0.00007	0.0191
TH	0.00790	0.08830	0.02710	0.07860	0.01170	0.01670	0.05380	0.07990	0.00250	-	0.00331	<0.00007	<0.00007
WCF	0.00840	0.06740	0.03090	0.07780	0.00720	0.01280	0.04420	0.05990	0.00800	0.00630	-	<0.00007	0.01626
WO	0.01850	0.11350	0.03220	0.06430	0.01540	0.03840	0.09040	0.08260	0.03780	0.03980	0.03930	-	<0.00007
WSL	0.00210	0.06560	0.02180	0.06580	0.00580	0.00410	0.05350	0.06540	0.00550	0.01780	0.00670	0.03140	-
Mean	0.02610	0.09105	0.04760	0.08584	0.02519	0.03160	0.06888	0.07534	0.02713	0.03238	0.03066	0.04996	0.02828

Table 10. Summary of analysis of molecular variance (AMOVA) analysis from two to six group hypotheses. Grouping with the highest V_a/V_b are included. Full population names are in Table 1. Iterations refer to the number of unique population arrangements for the designated number of groups tested.

# of Groups	Iterations/Group	Max. V_a/V_b *	Grouping *
2	72	0.474	A) NT, TH, GR, SQ, WCF, EC, LCO, LL, TEA, BN, DAY, AM, LC, MN, MOS, MCL, TCF, BL, SS B) WO, MC, SI, KT, NN, BC, KA, LAV, BAV, BIG, SPI, WSL, PM, LSG
3	11	1.133	A) WO, MC, SI, KT, NN, BC, KA, LAV, BAV, BIG, SPI, WSL, PM, LSG B) NT, TH, GR, SQ, WCF, EC, LCO, LL, TEA, BN, DAY, AM, LC, MN, BL, SS C) MOS, MCL, TCF
4	21	1.052	A) BAV, BIG, LAV, PM, SPI, WSL, KT, NN B) BN, DAY, LC, LCO, LL, SQ, TEA, GR, EC, TH, WCF, AM, MN, BL, SS, NT C) LSG, SI, WO, KA, MC, BC D) MOS, MCL, TCF
5	11	1.249	A) KA, LSG, MC, SI, WO, BC B) MCL, MOS, TCF C) NT, BL, MN, AM, LC, BN, DAY, LL, LCO, TEA, WCF, EC, GR, SQ, TH BAV, BIG, LAV, PM, KT, NN, WSL, D) SPI E) SS
6	11	1.376	A) KA, LSG, MC, SI, WO, BC B) MCL, MOS C) NT, BL, MN, AM, LC, BN, DAY, LL, LCO, TEA, WCF, EC, GR, SQ, TH BAV, BIG, LAV, PM, KT, NN, WSL, D) SPI E) SS F) TCF

* All iterations were significant both among and within putative groupings

Table 11. Average pairwise F_{ST} values within and among genetic units. For explanation of groupings see Table 8d.

Group	Within Group F_{ST}	Among Group F_{ST}
Group 1	0.0233	0.0474
Group 2	0.0198	0.0515
Group 3	0.0322	0.0722
Average	0.0251	0.0570

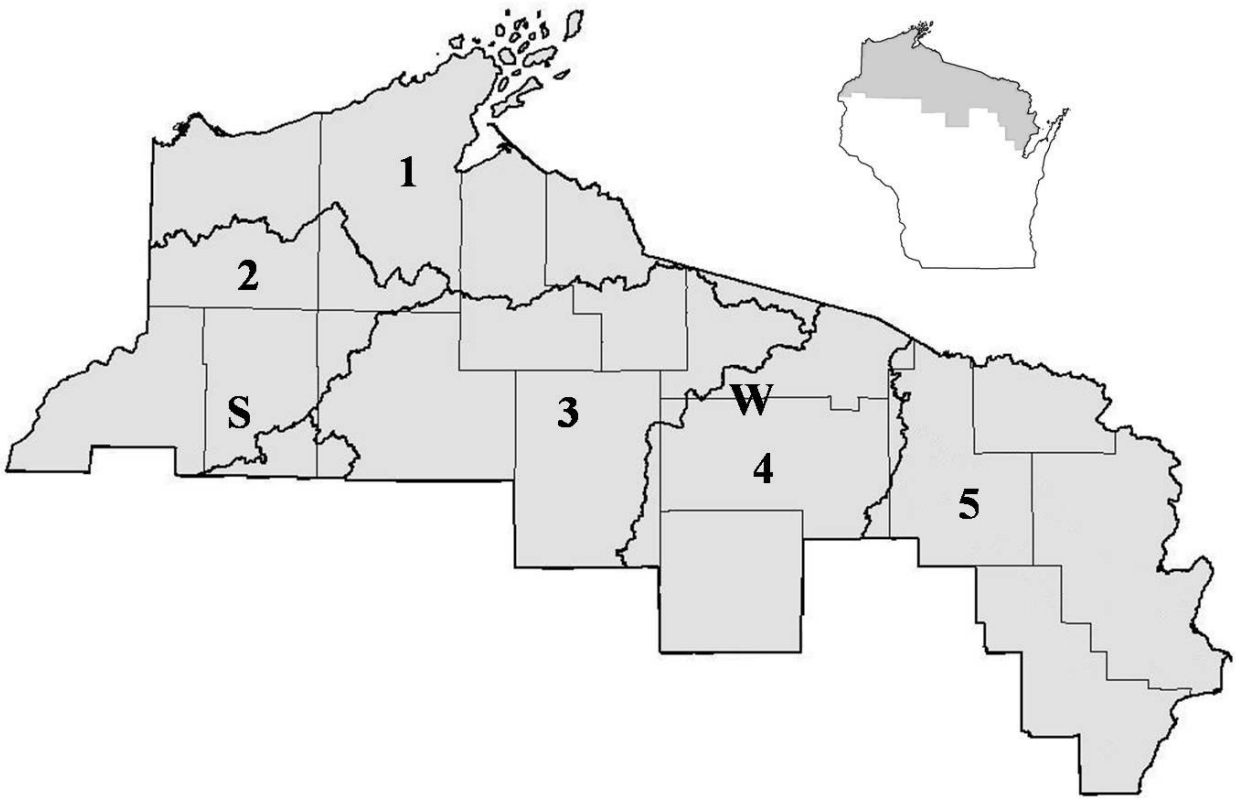


Figure 1. Map of northern Wisconsin encompassing native range and current management units (1=Lake Superior, 2=St. Croix, 3=upper Chippewa, 4=upper Wisconsin, 5=Green Bay) of muskellunge. Bold lines denote management unit boundaries while thin lines represent county boarders. Northern Wisconsin hatcheries include the Governor Tommy G. Thompson Hatchery in Spooner (denoted S) and Art Oehmcke Hatchery in Woodruff (denoted W).

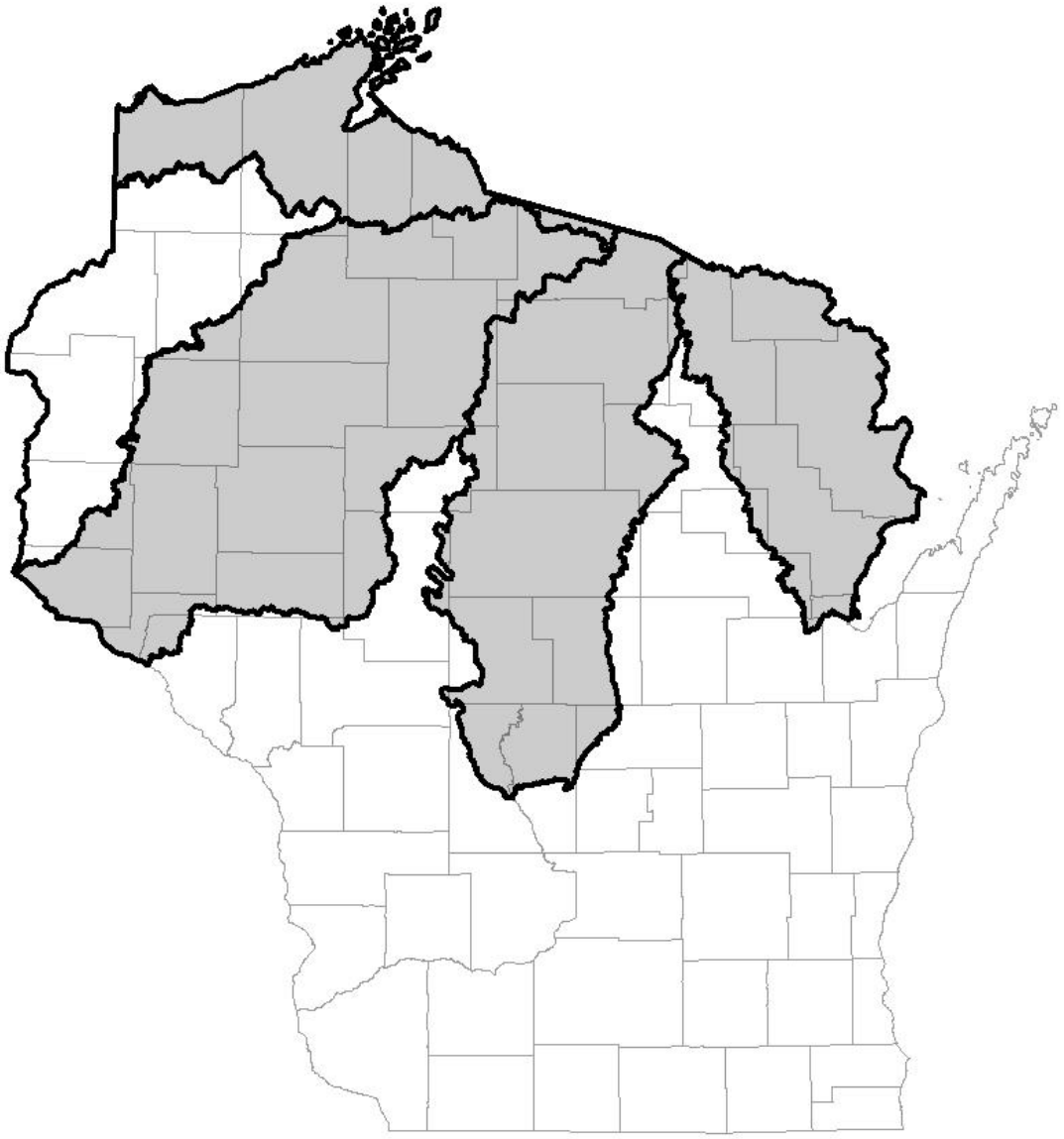


Figure 2. Native watershed basins of muskellunge in Wisconsin according to Becker (1983).

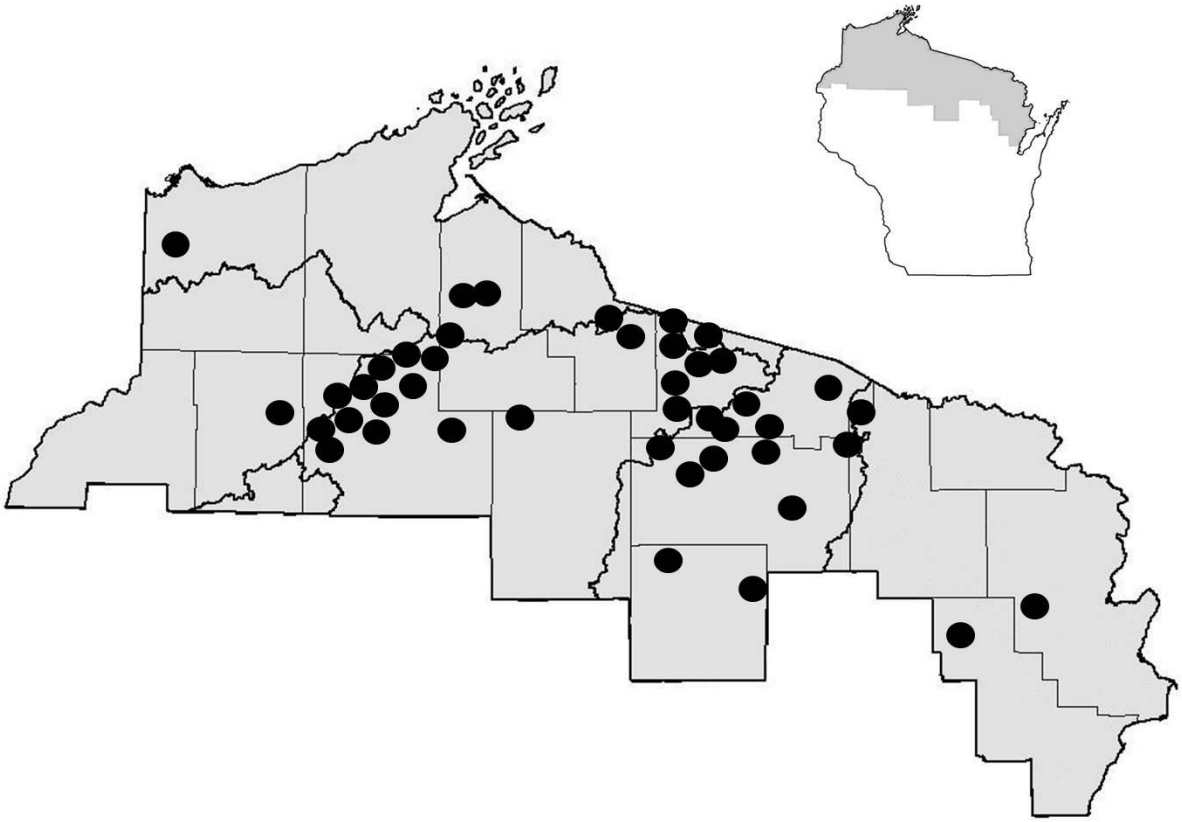


Figure 3. Location of 43 sample sites where samples were collected. Thin lines represent county boarders while bold lines indicate watershed boundaries. Refer to Figure 1 for watershed names.

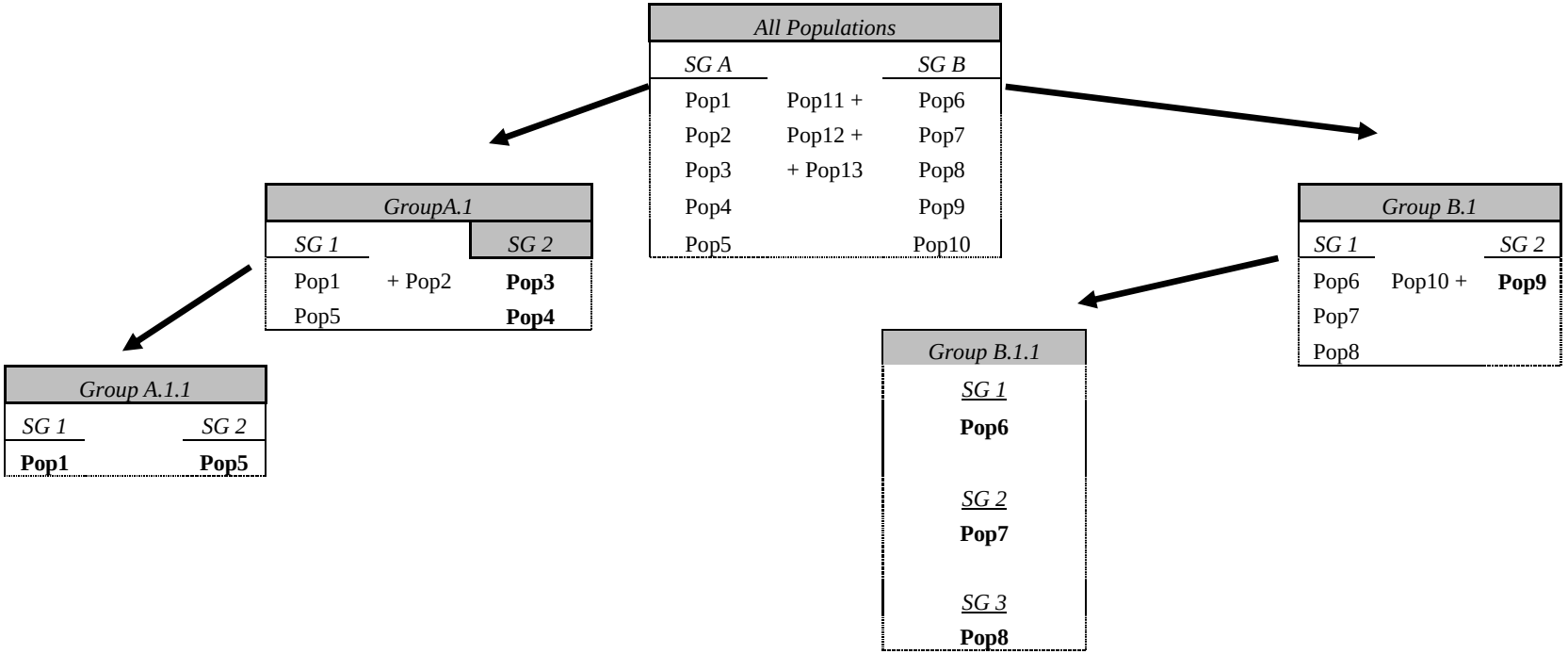
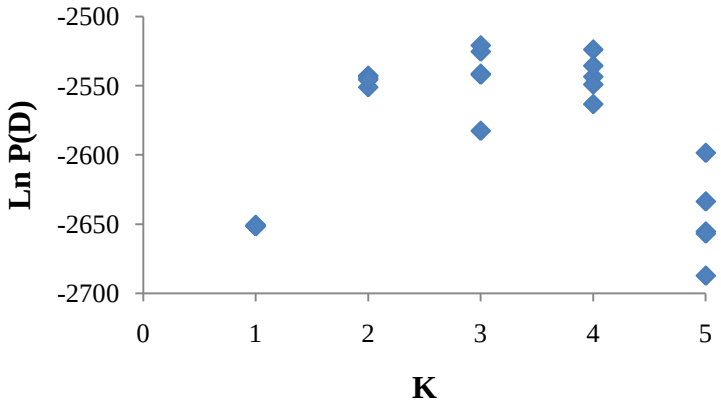
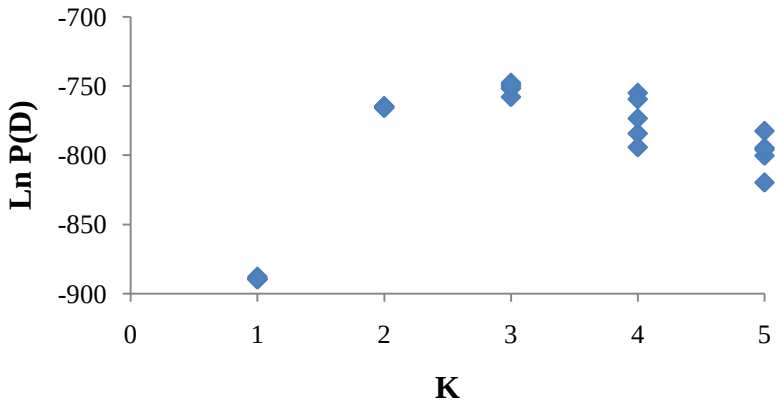


Figure 4. Hypothetical model for the Evanno et al. (2005) method of GSI using 15 populations. Gray boxes represent analyses in STRUCTURE 2.2 and bold populations represent unique gene pools. Populations with a (+) indicate partial assignment to a group and were assumed to be independent gene pools. Box labeled "All Populations" is initial partition in STRUCTURE 2.2 when K = 1-10 with two being the most likely K value. Populations 1-5 assign to Group A with ≥ 0.60 confidence while population 13 assigns to Group A with < 0.60 confidence. Similarly populations 6-10 assign to Group B and populations 11 and 12 partially assign to Group B. Group A.1 represents analysis of Group A with two being the most likely K value. SG 1 was then tested as Group A.1.1 with populations 1 and 5 grouping independently from each other. Population 2 partially assigned to SG1. SG 2 was composed of population 3 and 4. When tested for K = 1-3, one gene pool was observed. Group B.1 consisted of Group B and two was the most likely K value. SG 1, composed of populations 6,7, and 8 were tested for K = 1-4 with three being the most likely K value and each population assigning independently. Population 10 partially assigned to SG 2, which was composed exclusively of population 9. Fourteen unique gene pools were identified in this scenario.

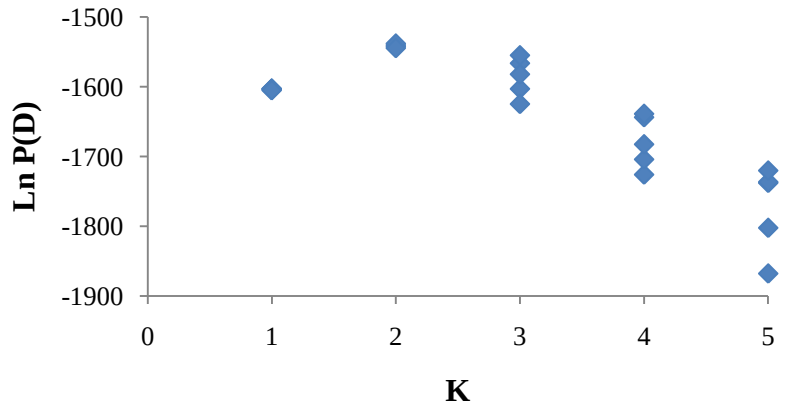
A) Lac Courte Oreilles



B) Archibald Lake



C) Somo Lake



D) Lake Tomahawk

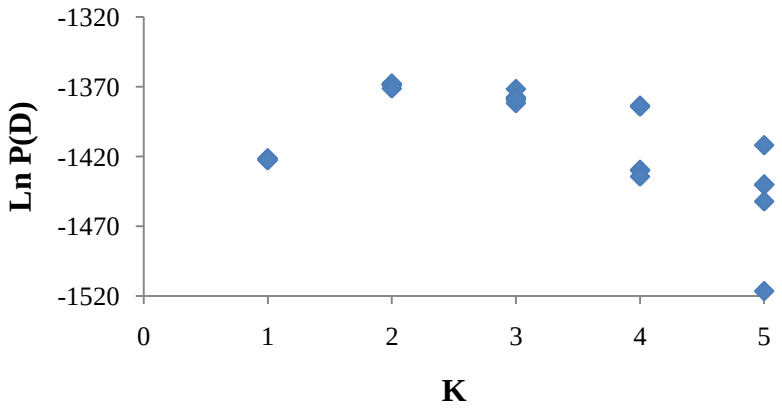
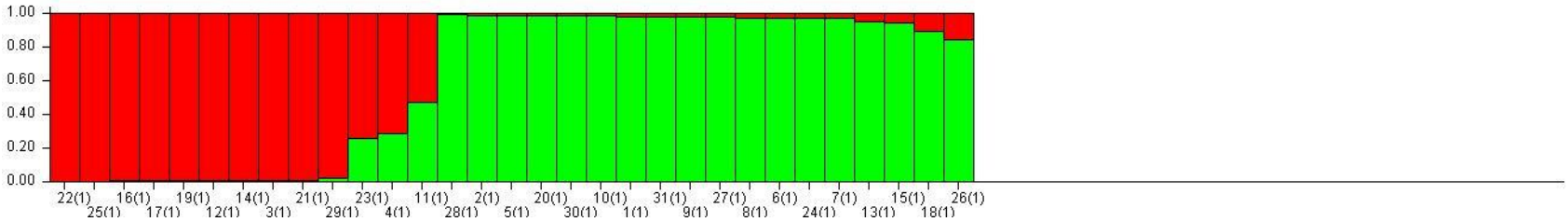


Figure 5. Ln P(D) vs. K for a) Archibald Lake, b) Lac Courte Oreilles, c) Somo Lake, and d) Lake Tomahawk from STRUCTURE 2.2. There are 5 replicates for each putative K value and asymptotes on a graph are the most likely K value for that population.

A) Archibald Lake



B) Lac Courte Oreilles

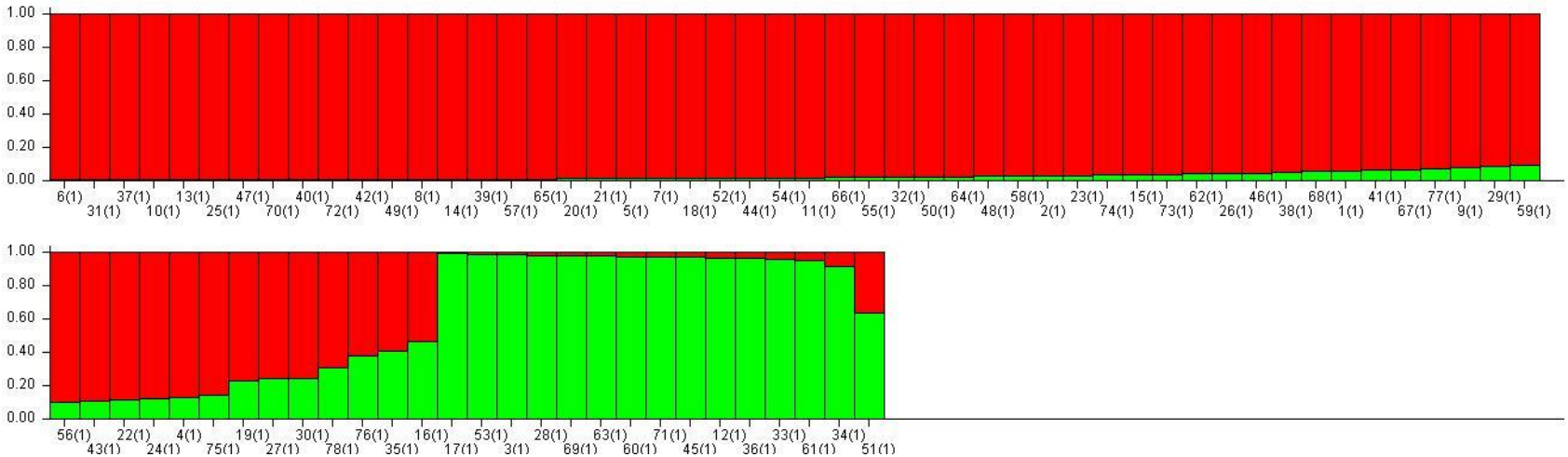
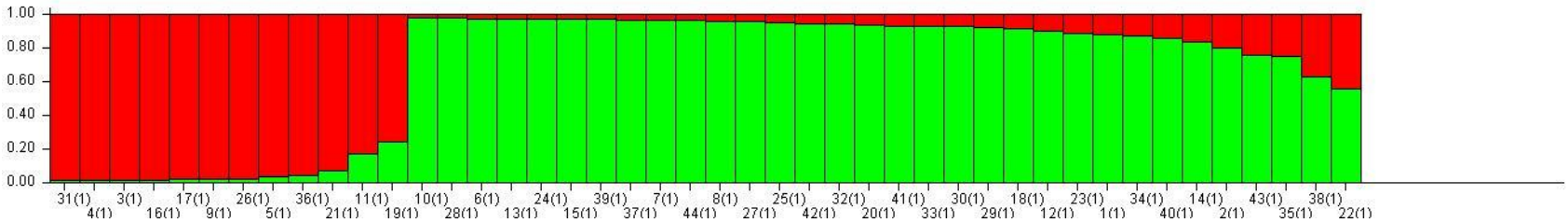


Figure 6. Bar plots from STRUCTURE 2.2 for a) Archibald Lake, b) Lac Courte Oreilles, c) Somo Lake, and d) Lake Tomahawk when K is 2. Vertical boxes represent individual muskellunge (individual identification below graph) and probability of each genotype belonging to Group 1 (red) or Group 2 (green).

C) Somo Lake



D) Lake Tomahawk

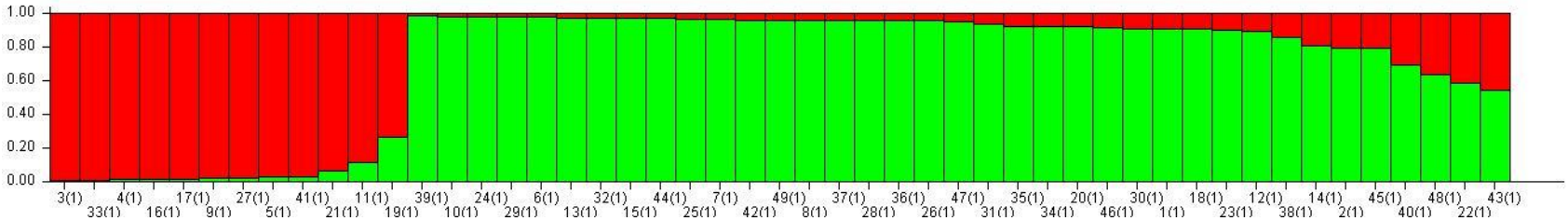


Figure 6. (Continued).

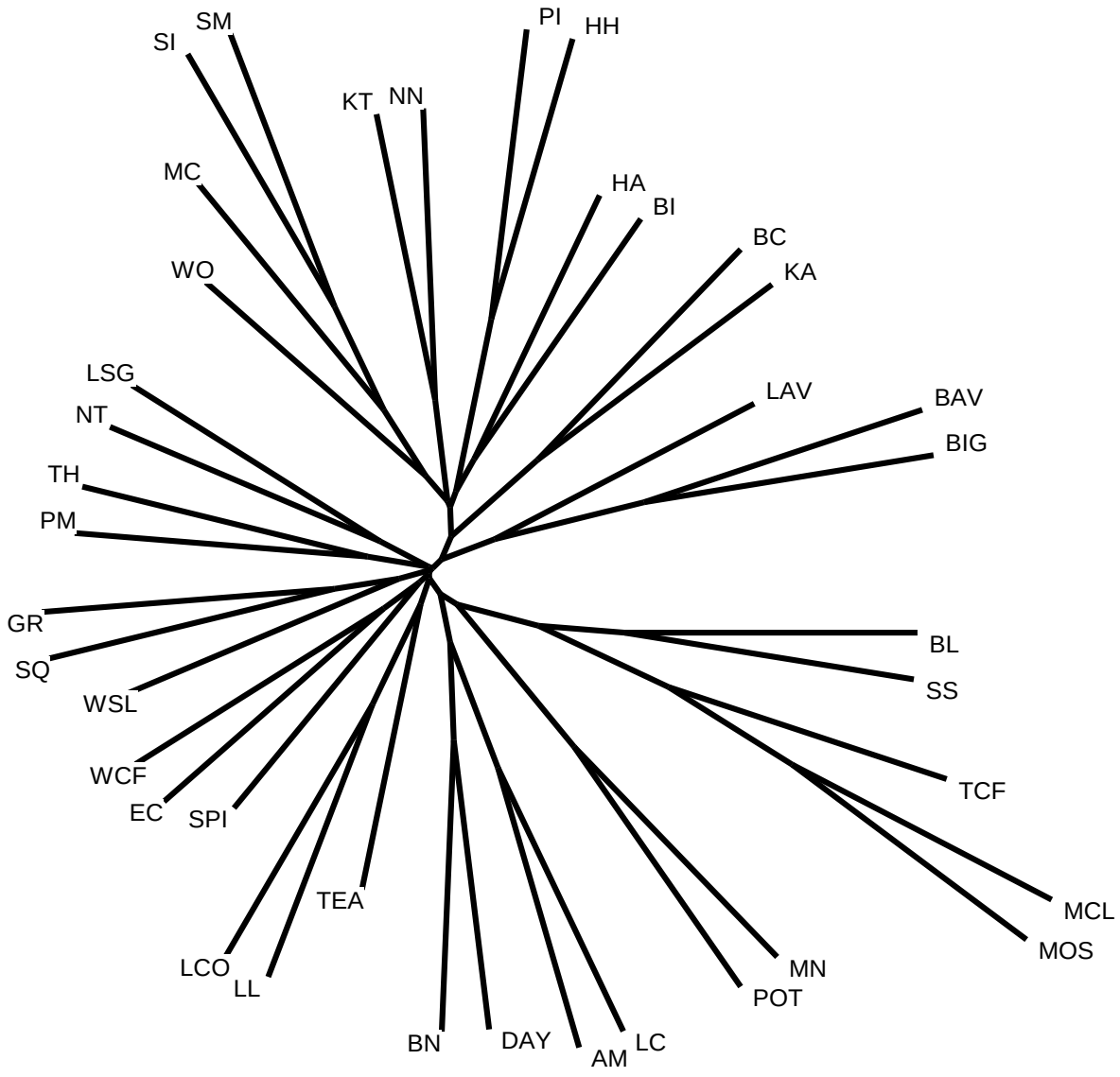


Figure 7. Unrooted neighbor joining tree based on Cavalli-Sforza and Edwards (1967) chord distance (D_c). Full population names are in Table 1.

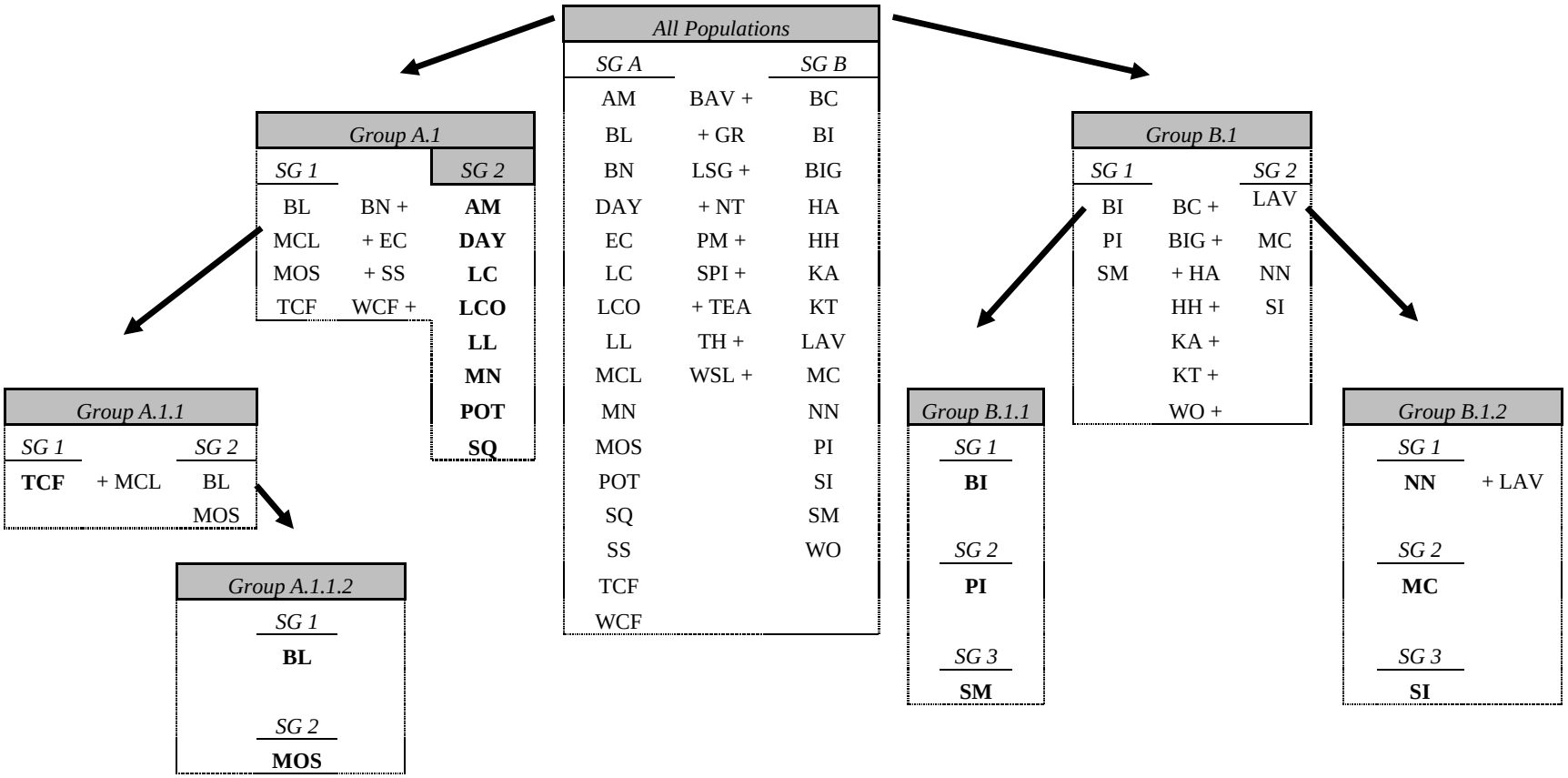


Figure 8. Results from STRUCTURE 2.2 following the Coulon et al. (2008) method of assignment. Gray boxes represent putative clusters tested in STRUCTURE 2.2 while number of sub-groups (SG) represent correct K values for each group. Populations with a (+) indicate most likely inclusion to a group, however <0.60 probability of inclusion was attained. Bolded populations/groupings are stable (K = 1) following Evanno et al. (2005) method.

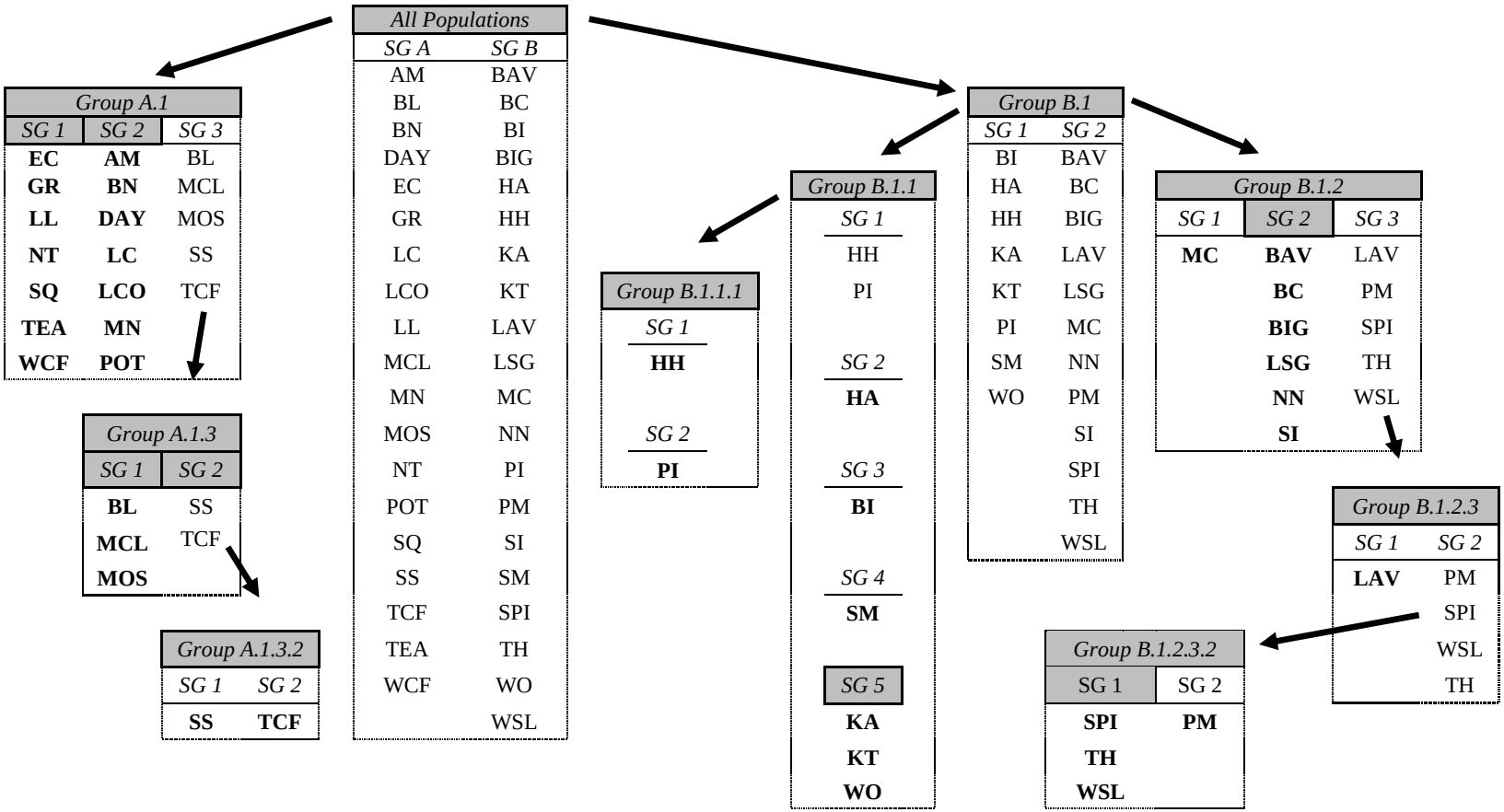


Figure 9. Results from STRUCTURE 2.2 following the absolute method of assignment. Gray boxes represent putative clusters tested in STRUCTURE 2.2 while number of sub-groups (SG) represent correct K values for each group. Bolded populations/groupings are stable (K = 1) following Evanno et al. (2005) method.

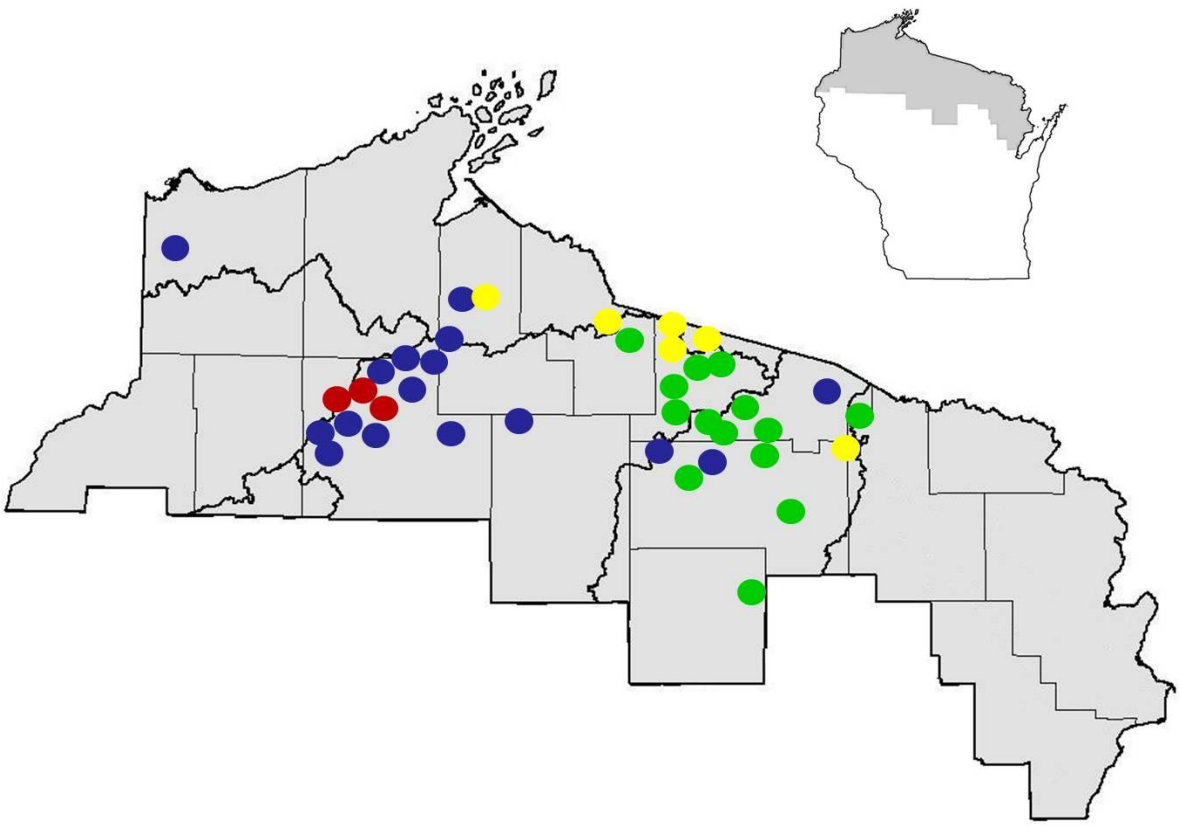


Figure 10. Genetic management units (GMUs) identified through AMOVA, V_a/V_b, STRUCTURE, and F-statistics (Wisconsin River Genetic Unit; Green, Upper Chippewa River Genetic Unit; Blue, Central Chippewa River Genetic Unit; Red). Explanations are in Table 8d. Populations omitted from GMU analysis are in Yellow.

Appendix 1. Allele frequencies for each population at each locus. See Table 1 for population abbreviations.

Locus/ Alleles	Populations																				
Ema-A5	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
214	1.0	38.7	15.9	7.0	20.4	17.5	13.0	0.0	0.0	3.2	3.0	4.2	11.8	2.9	2.2	9.1	2.4	9.4	0.0	3.6	7.9	6.3
224	80.0	54.8	72.7	82.0	44.4	67.5	73.0	88.1	82.1	80.9	82.0	80.2	67.6	72.9	63.0	83.3	64.6	70.8	88.1	82.1	84.2	79.2
226	19.0	6.5	11.4	11.0	35.2	15.0	14.0	11.9	17.9	16.0	15.0	15.6	20.6	24.3	34.8	7.6	32.9	19.8	11.9	14.3	7.9	14.6
228	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Locus/ Alleles	Populations																				
Ema-A5	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL	
214	8.5	1.0	1.0	1.1	6.7	7.6	12.9	10.9	4.5	4.4	8.3	3.9	6.3	3.9	0.0	2.2	10.4	18.4	6.6	3.1	2.4	
224	75.4	84.7	90.0	88.0	67.8	83.3	62.9	75.0	95.5	70.0	73.3	73.7	79.2	80.3	89.7	81.5	77.1	71.4	77.6	83.7	70.7	
226	16.1	14.3	9.0	10.9	25.6	9.1	24.2	14.1	0.0	25.6	18.3	22.4	14.6	15.8	10.3	16.3	11.5	10.2	15.8	13.3	22.0	
228	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	4.9	
Locus/ Alleles	Populations																				
Ema-A10	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
152	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
154	1.0	0.0	0.0	1.0	0.0	0.0	0.0	2.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	2.4	0.0	0.0	0.0
156	1.0	0.0	11.4	1.0	0.0	1.3	0.0	2.4	6.1	3.2	4.0	1.0	0.0	0.0	2.2	0.0	0.0	0.0	11.9	2.7	2.6	1.0
158	81.0	83.9	88.6	80.0	62.9	96.3	85.0	88.1	76.8	74.5	85.0	89.6	75.7	94.4	95.7	92.4	87.8	93.0	76.2	82.1	78.1	79.6
160	1.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	1.1	0.0	0.0	1.4	0.0	0.0	0.0	1.2	0.0	0.0	0.0	0.0	0.0
162	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
164	16.0	16.1	0.0	18.0	37.1	2.5	13.0	7.1	17.1	21.3	11.0	9.4	20.0	5.6	2.2	7.6	11.0	6.1	9.5	15.2	19.3	19.4

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-A10	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
152	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
154	13.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.2	13.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.1	1.0
156	7.8	5.1	18.0	4.3	2.2	4.4	4.8	1.1	25.0	0.0	0.0	0.0	4.2	1.3	2.5	7.6	1.0	0.0	2.5	0.0	1.0
158	71.6	90.8	74.0	90.4	88.9	80.9	95.2	85.9	47.7	85.9	86.2	85.0	91.7	80.3	80.0	89.1	88.5	83.7	83.8	90.8	78.8
160	0.0	0.0	0.0	0.0	2.2	1.5	0.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	1.0	3.1	0.0	0.0	0.0
162	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
164	6.9	4.1	8.0	5.3	6.7	13.2	0.0	13.0	27.3	9.8	0.0	15.0	4.2	18.4	17.5	3.3	9.4	13.3	13.8	6.1	19.2

Locus/ Alleles	Populations																					
Ema-A11	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
130	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	0.0	0.0	0.0	0.0	0.0
134	23.0	21.0	27.3	19.0	11.1	3.8	19.0	20.5	19.0	13.0	6.0	18.8	28.6	29.2	23.9	13.6	6.1	16.0	7.1	13.4	14.0	16.0
136	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
138	2.0	0.0	4.5	0.0	0.0	1.3	0.0	0.0	4.8	3.3	1.0	3.1	1.4	0.0	0.0	3.0	0.0	1.9	2.4	0.0	2.6	2.1
142	75.0	79.0	68.2	81.0	88.9	95.0	81.0	79.5	72.6	83.7	92.0	75.0	70.0	70.8	76.1	83.3	92.7	82.1	90.5	82.1	78.9	80.9
144	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.6	0.0	1.0	2.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	4.5	4.4	1.1

Locus/ Alleles	Populations																				
Ema-A11	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
130	7.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.0	0.0
134	29.8	9.2	43.0	3.2	14.8	19.1	14.5	17.4	36.4	32.6	45.2	12.5	18.8	11.5	5.1	20.7	21.9	11.2	12.5	15.0	14.6
136	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	8.7	0.0	0.0	0.0	0.0	0.0
138	0.9	1.0	0.0	1.1	10.2	4.4	0.0	3.3	0.0	0.0	0.0	1.1	2.1	2.6	0.0	1.1	6.3	2.0	0.0	9.0	1.2
142	62.3	87.8	57.0	95.7	75.0	73.5	85.5	79.3	63.6	67.4	54.8	86.4	79.2	85.9	93.6	68.5	70.8	84.7	83.8	73.0	84.1
144	0.0	1.0	0.0	0.0	0.0	2.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	1.1	1.0	2.0	3.8	0.0	0.0

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-A102	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
129	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
131	0.0	0.0	20.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
133	0.0	0.0	5.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
135	62.0	16.1	57.5	30.0	33.3	17.5	35.0	45.0	48.8	51.1	45.0	37.5	51.4	27.8	23.9	37.5	13.4	38.2	52.4	44.5	40.2	41.5
137	38.0	83.9	17.5	70.0	66.7	82.5	64.0	55.0	51.2	48.9	55.0	62.5	45.7	72.2	76.1	62.5	86.6	61.8	47.6	55.5	59.8	58.5
139	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Locus/ Alleles	Populations																				
Ema-A102	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL	
129	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
131	1.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
133	4.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	8.1	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	
135	30.2	40.8	47.0	35.1	26.7	48.5	4.8	31.1	22.7	22.8	4.8	35.2	20.0	34.6	65.4	30.4	39.6	46.9	40.0	19.0	26.8	
137	62.9	59.2	53.0	64.9	73.3	51.5	95.2	68.9	77.3	77.2	87.1	64.8	80.0	65.4	34.6	69.6	60.4	52.1	60.0	81.0	73.2	
139	0.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

Locus/ Alleles	Populations																					
Ema-A104	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
161	20.0	24.1	13.6	14.0	35.2	23.8	11.0	25.0	2.4	13.0	6.0	19.8	15.7	8.3	6.5	37.1	12.2	19.3	7.1	10.9	7.0	23.8
163	41.0	37.9	38.6	46.0	25.9	55.0	46.0	31.8	69.0	45.7	49.0	49.0	50.0	33.3	21.7	33.9	31.7	28.9	50.0	40.9	46.5	31.0
165	38.0	37.9	47.7	38.0	37.0	21.3	43.0	43.2	26.2	39.1	43.0	30.2	34.3	58.3	71.7	29.0	56.1	50.9	42.9	45.5	44.7	45.2
167	1.0	0.0	0.0	2.0	1.9	0.0	0.0	0.0	2.4	1.1	2.0	1.0	0.0	0.0	0.0	0.0	0.0	0.9	0.0	2.7	1.8	0.0
169	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Locus/ Alleles	Populations																				
Ema-A104	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL	
161	18.4	11.2	4.0	7.4	11.1	23.5	21.0	18.5	11.4	21.7	22.4	21.6	16.0	11.4	5.1	5.4	10.4	12.2	25.0	21.0	19.5	
163	47.4	75.5	39.0	70.2	21.1	47.1	33.9	35.9	63.6	39.1	51.7	29.5	52.0	44.3	62.8	89.1	35.4	44.9	43.8	35.0	32.9	
165	29.8	12.2	54.0	22.3	67.8	29.4	45.2	43.5	25.0	39.1	25.9	48.9	32.0	44.3	26.9	5.4	52.1	42.9	31.3	44.0	46.3	
167	0.9	1.0	1.0	0.0	0.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	5.1	0.0	2.1	0.0	0.0	0.0	1.2	
169	3.5	0.0	2.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

Appendix 1. (Continued).

Locus/ Alleles	Populations																					
Ema-B110	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
181	66.3	25.8	38.6	51.0	40.7	27.5	45.9	79.5	61.0	56.5	54.0	59.4	54.3	37.5	34.8	50.0	47.6	50.9	64.3	57.1	51.8	55.3
183	11.2	40.3	29.5	11.0	11.1	40.0	13.3	11.4	14.6	10.9	20.0	16.7	10.0	47.2	4.3	10.6	14.6	15.8	9.5	15.2	16.7	9.6
185	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
189	22.4	33.9	31.8	38.0	48.1	32.5	40.8	9.1	24.4	32.6	26.0	24.0	34.3	15.3	60.9	39.4	37.8	33.3	26.2	27.7	31.6	35.1
Locus/ Alleles	Populations																					
Ema-B110	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL	
181	63.4	59.2	56.0	70.2	46.6	63.2	18.3	45.7	88.6	56.7	71.0	44.3	52.0	56.4	87.2	83.7	56.5	38.8	56.4	47.0	62.2	
183	1.8	32.7	6.0	16.0	15.9	7.4	6.7	9.8	0.0	7.8	0.0	23.9	20.0	9.0	9.0	4.3	15.2	25.5	24.4	5.0	8.5	
185	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
189	34.8	8.2	38.0	13.8	37.5	29.4	75.0	44.6	11.4	35.6	29.0	31.8	28.0	34.6	3.8	12.0	28.3	35.7	19.2	48.0	29.3	
Locus/ Alleles	Populations																					
Ema-B120	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
234	54.0	80.6	54.8	69.0	74.1	97.5	79.6	40.9	57.3	53.2	50.0	63.8	54.3	72.2	76.1	82.8	82.9	66.3	61.9	53.6	50.0	67.0
236	46.0	19.4	45.2	31.0	25.9	2.5	20.4	59.1	42.7	46.8	50.0	36.2	45.7	27.8	23.9	17.2	17.1	33.7	38.1	46.4	50.0	33.0
Locus/ Alleles	Populations																					
Ema-B120	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL	
234	86.0	82.7	63.3	91.5	79.5	70.6	74.2	65.6	43.2	87.8	100.0	62.5	76.0	52.6	63.2	69.6	62.5	67.7	60.0	88.8	61.0	
236	14.0	17.3	36.7	8.5	20.5	29.4	25.8	34.4	56.8	12.2	0.0	37.5	24.0	47.4	36.8	30.4	37.5	32.3	40.0	11.2	39.0	
Locus/ Alleles	Populations																					
Ema-C1	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
201	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
205	2.0	0.0	13.6	0.0	0.0	2.5	1.0	4.5	4.8	2.1	12.0	2.1	0.0	0.0	2.2	0.0	0.0	0.0	2.4	5.5	4.4	3.6
209	6.0	8.6	0.0	5.0	7.4	6.3	9.2	13.6	1.2	4.3	3.0	9.4	4.3	0.0	39.1	3.2	11.0	6.1	14.3	19.1	7.9	15.5
213	91.0	87.9	81.8	89.0	85.2	83.8	84.7	81.8	91.7	89.4	82.0	80.2	88.6	94.4	52.2	80.6	68.3	83.3	73.8	74.5	80.7	75.0
217	0.0	3.4	4.5	6.0	7.4	7.5	5.1	0.0	2.4	3.2	3.0	8.3	4.3	5.6	6.5	16.1	20.7	10.5	9.5	0.9	6.1	4.8
221	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	1.2

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-C1	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
201	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
205	6.8	3.1	0.0	18.1	3.3	1.5	0.0	2.2	0.0	0.0	1.7	2.3	0.0	2.7	3.9	1.1	4.2	0.0	5.0	0.0	7.3
209	5.1	38.8	3.0	19.1	0.0	14.7	0.0	8.7	0.0	3.3	0.0	4.5	12.0	6.8	19.7	33.7	5.2	3.1	6.3	13.0	4.9
213	79.7	55.1	96.0	57.4	72.2	79.4	91.9	82.6	84.1	92.4	98.3	88.6	84.0	87.8	76.3	64.1	89.6	94.9	81.3	74.0	78.0
217	8.5	3.1	1.0	5.3	24.4	4.4	8.1	6.5	15.9	4.3	0.0	4.5	4.0	2.7	0.0	1.1	1.0	2.0	6.3	13.0	9.8
221	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	0.0	0.0

Locus/ Alleles	Populations																					
Ema-D5	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
201	0.0	0.0	0.0	0.0	0.0	1.3	0.0	0.0	1.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
205	0.0	0.0	0.0	0.0	0.0	30.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	1.3	0.9	0.0	0.0	0.0	1.0
209	0.0	1.7	0.0	5.0	0.0	5.0	4.2	0.0	0.0	2.1	0.0	0.0	1.4	0.0	0.0	1.5	10.0	8.6	0.0	0.9	2.7	5.2
213	10.0	5.0	9.1	12.0	0.0	2.5	8.3	0.0	4.8	13.8	19.0	7.3	11.4	3.0	0.0	10.6	5.0	12.1	11.9	15.7	5.4	7.3
217	4.0	11.7	0.0	2.0	11.1	7.5	4.2	0.0	1.2	2.1	1.0	2.1	4.3	18.2	0.0	3.0	0.0	4.3	0.0	2.8	3.6	3.1
221	9.0	31.7	6.8	6.0	5.6	10.0	5.2	15.0	1.2	5.3	4.0	7.3	11.4	4.5	2.3	3.0	6.3	6.0	7.1	0.9	5.4	8.3
225	5.0	1.7	2.3	1.0	1.9	12.5	1.0	7.5	3.6	2.1	5.0	5.2	0.0	0.0	0.0	0.0	1.3	1.7	2.4	4.6	2.7	2.1
229	2.0	0.0	6.8	1.0	0.0	0.0	1.0	2.5	2.4	3.2	1.0	2.1	4.3	9.1	0.0	0.0	5.0	0.9	0.0	0.0	2.7	4.2
233	5.0	0.0	0.0	2.0	1.9	0.0	0.0	2.5	6.0	4.3	3.0	4.2	1.4	4.5	0.0	1.5	2.5	3.4	7.1	3.7	4.5	8.3
237	1.0	0.0	2.3	4.0	1.9	2.5	5.2	10.0	2.4	2.1	0.0	10.4	4.3	1.5	18.2	9.1	10.0	1.7	2.4	2.8	2.7	7.3
241	2.0	0.0	4.5	9.0	13.0	3.8	7.3	0.0	4.8	4.3	1.0	5.2	2.9	27.3	18.2	6.1	5.0	1.7	0.0	6.5	7.1	9.4
245	9.0	13.3	15.9	19.0	22.2	7.5	16.7	2.5	17.9	9.6	18.0	13.5	5.7	9.1	11.4	16.7	8.8	15.5	9.5	14.8	20.5	16.7
249	11.0	3.3	6.8	12.0	3.7	5.0	15.6	2.5	13.1	11.7	19.0	9.4	12.9	12.1	6.8	6.1	10.0	12.9	28.6	13.9	7.1	10.4
253	9.0	11.7	15.9	11.0	14.8	10.0	17.7	5.0	9.5	11.7	10.0	10.4	11.4	3.0	13.6	18.2	15.0	13.8	7.1	12.0	10.7	7.3
257	6.0	3.3	6.8	4.0	0.0	2.5	3.1	17.5	13.1	3.2	5.0	1.0	12.9	1.5	20.5	4.5	11.3	6.9	0.0	4.6	8.0	1.0
261	5.0	0.0	2.3	2.0	3.7	0.0	2.1	2.5	0.0	4.3	0.0	4.2	1.4	1.5	4.5	10.6	0.0	2.6	2.4	0.9	5.4	3.1
265	8.0	8.3	9.1	5.0	5.6	0.0	5.2	5.0	6.0	7.4	6.0	7.3	5.7	0.0	4.5	4.5	0.0	2.6	7.1	9.3	5.4	0.0
269	3.0	3.3	6.8	1.0	14.8	0.0	1.0	2.5	1.2	1.1	3.0	1.0	4.3	1.5	0.0	1.5	5.0	0.9	2.4	1.9	1.8	3.1
273	11.0	5.0	4.5	0.0	0.0	0.0	0.0	0.0	8.3	7.4	5.0	3.1	4.3	1.5	0.0	0.0	1.3	0.0	11.9	3.7	3.6	1.0
277	0.0	0.0	0.0	1.0	0.0	0.0	2.1	5.0	0.0	2.1	0.0	5.2	0.0	0.0	0.0	0.0	2.5	1.7	0.0	0.0	0.9	0.0
281	0.0	0.0	0.0	1.0	0.0	0.0	0.0	20.0	0.0	1.1	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.9	0.0	0.9	0.0	1.0
285	0.0	0.0	0.0	2.0	0.0	0.0	0.0	0.0	3.6	1.1	0.0	1.0	0.0	0.0	0.0	1.5	0.0	0.9	0.0	0.0	0.0	0.0
289	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-D5	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
201	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.4	0.0	0.0	0.0	0.0	2.1	0.0	0.0	0.0	0.0
205	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0
209	0.0	0.0	2.0	0.0	6.3	2.9	0.0	3.3	0.0	10.9	0.0	4.5	0.0	1.3	1.3	0.0	2.1	4.1	2.5	5.1	0.0
213	3.8	6.3	8.0	7.8	11.3	7.4	0.0	18.5	4.8	12.0	5.6	8.0	12.5	5.1	6.6	2.3	10.4	14.3	8.8	9.2	11.0
217	1.0	2.1	0.0	5.6	0.0	4.4	0.0	2.2	0.0	3.3	0.0	6.8	4.2	0.0	0.0	2.3	0.0	2.0	1.3	6.1	3.7
221	1.9	4.2	3.0	18.9	6.3	5.9	13.3	3.3	0.0	3.3	18.5	3.4	4.2	15.4	1.3	3.4	4.2	7.1	8.8	4.1	4.9
225	0.0	5.2	4.0	14.4	2.5	1.5	1.7	3.3	4.8	0.0	0.0	2.3	4.2	1.3	0.0	2.3	1.0	3.1	1.3	3.1	0.0
229	5.8	4.2	1.0	0.0	2.5	1.5	0.0	2.2	0.0	6.5	0.0	4.5	2.1	6.4	0.0	10.2	1.0	0.0	5.0	3.1	1.2
233	2.9	2.1	1.0	0.0	3.8	7.4	0.0	3.3	0.0	0.0	0.0	2.3	6.3	5.1	7.9	5.7	4.2	1.0	2.5	1.0	2.4
237	2.9	11.5	3.0	2.2	2.5	1.5	6.7	4.3	0.0	3.3	0.0	2.3	2.1	1.3	10.5	17.0	1.0	2.0	7.5	5.1	6.1
241	5.8	18.8	3.0	11.1	1.3	4.4	10.0	3.3	7.1	18.5	14.8	4.5	6.3	7.7	3.9	18.2	4.2	6.1	12.5	11.2	6.1
245	13.5	13.5	20.0	3.3	26.3	22.1	0.0	15.2	45.2	7.6	3.7	9.1	18.8	9.0	7.9	6.8	14.6	15.3	7.5	8.2	7.3
249	6.7	1.0	15.0	2.2	12.5	17.6	6.7	9.8	0.0	13.0	0.0	20.5	12.5	14.1	11.8	3.4	10.4	10.2	10.0	14.3	11.0
253	12.5	8.3	12.0	0.0	13.8	7.4	36.7	15.2	4.8	12.0	24.1	10.2	8.3	9.0	14.5	13.6	12.5	6.1	8.8	15.3	11.0
257	32.7	18.8	16.0	20.0	3.8	7.4	15.0	5.4	4.8	3.3	13.0	3.4	4.2	7.7	9.2	5.7	10.4	7.1	5.0	2.0	11.0
261	2.9	0.0	1.0	6.7	0.0	0.0	5.0	2.2	2.4	1.1	0.0	1.1	0.0	1.3	2.6	5.7	5.2	0.0	0.0	3.1	4.9
265	1.0	1.0	7.0	0.0	0.0	2.9	3.3	6.5	9.5	3.3	3.7	8.0	4.2	12.8	6.6	1.1	6.3	15.3	3.8	5.1	3.7
269	0.0	0.0	0.0	2.2	2.5	1.5	1.7	0.0	11.9	0.0	0.0	1.1	8.3	1.3	6.6	0.0	5.2	2.0	6.3	0.0	7.3
273	5.8	2.1	3.0	2.2	3.8	2.9	0.0	2.2	0.0	0.0	1.9	2.3	2.1	1.3	2.6	1.1	5.2	4.1	8.8	3.1	6.1
277	1.0	1.0	1.0	3.3	1.3	0.0	0.0	0.0	4.8	0.0	0.0	2.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2
281	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	14.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2
285	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	0.0	0.0	0.0	0.0	3.9	1.1	0.0	0.0	0.0	0.0	0.0
289	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.6	0.0	0.0	0.0	0.0	0.0	0.0

Appendix 1. (Continued).

Locus/ Alleles	Populations																					
Ema-D6	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
165	20.0	9.7	4.5	19.0	29.6	37.5	19.8	27.8	25.6	33.0	17.0	26.0	32.4	34.3	28.3	33.3	31.7	25.0	14.3	27.8	25.9	21.9
177	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
213	2.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	1.4	0.0	0.0	0.0	0.0	7.1	0.0	0.0	0.0
217	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	1.5	1.4	0.0	0.0	0.0	0.0	0.0	0.9	1.8	0.0
221	0.0	6.5	0.0	0.0	3.7	0.0	0.0	0.0	0.0	0.0	0.0	4.2	0.0	1.4	0.0	0.0	0.0	0.9	0.0	0.9	0.9	1.0
225	2.0	0.0	9.1	2.0	1.9	0.0	0.0	19.4	2.4	1.1	8.0	11.5	0.0	1.4	0.0	6.1	0.0	1.7	0.0	0.9	0.0	1.0
229	20.0	35.5	18.2	28.0	13.0	2.5	18.8	5.6	24.4	24.5	38.0	17.7	25.0	12.9	6.5	12.1	13.4	28.4	31.0	20.4	25.9	22.9
233	8.0	1.6	11.4	7.0	11.1	11.3	11.5	41.7	9.8	8.5	5.0	9.4	8.8	4.3	0.0	24.2	11.0	6.0	4.8	9.3	8.0	13.5
237	18.0	27.4	25.0	20.0	24.1	3.8	22.9	0.0	12.2	7.4	14.0	11.5	8.8	10.0	2.2	16.7	4.9	12.1	9.5	16.7	13.4	19.8
241	9.0	1.6	9.1	9.0	11.1	8.8	9.4	0.0	9.8	14.9	6.0	4.2	17.6	12.9	15.2	4.5	29.3	12.9	4.8	15.7	13.4	6.3
245	2.0	0.0	2.3	7.0	1.9	11.3	9.4	0.0	4.9	7.4	3.0	6.3	2.9	15.7	19.6	0.0	1.2	7.8	2.4	3.7	4.5	3.1
249	11.0	17.7	13.6	3.0	3.7	6.3	3.1	2.8	2.4	2.1	5.0	1.0	1.5	0.0	26.1	3.0	4.9	5.2	14.3	1.9	2.7	9.4
253	3.0	0.0	2.3	5.0	0.0	3.8	4.2	2.8	3.7	0.0	0.0	3.1	0.0	4.3	0.0	0.0	2.4	0.0	2.4	1.9	1.8	1.0
257	4.0	0.0	2.3	0.0	0.0	0.0	1.0	0.0	4.9	1.1	2.0	3.1	0.0	0.0	2.2	0.0	0.0	0.0	2.4	0.0	1.8	0.0
261	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	4.8	0.0	0.0	0.0
265	0.0	0.0	2.3	0.0	0.0	1.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.4	0.0	0.0	0.0
269	0.0	0.0	0.0	0.0	0.0	13.8	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
277	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	0.0	0.0	0.0	0.0	0.0

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-D6	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
165	23.3	44.8	36.7	28.9	14.4	36.4	3.2	23.9	52.4	20.7	35.5	34.1	26.0	29.5	28.4	37.8	26.0	23.5	23.8	23.0	22.0
177	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
213	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
217	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	1.0	1.3	0.0	0.0
221	0.0	0.0	0.0	0.0	3.3	1.5	0.0	3.3	0.0	1.1	0.0	1.1	4.0	0.0	1.4	0.0	2.1	2.0	0.0	0.0	0.0
225	0.0	5.2	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	1.1	2.0	2.6	0.0	0.0	2.1	0.0	2.5	0.0	1.2
229	19.0	1.0	23.5	1.1	51.1	22.7	12.9	23.9	11.9	30.4	9.7	11.4	18.0	25.6	12.2	10.0	26.0	21.4	20.0	9.0	24.4
233	1.7	11.5	3.1	22.2	4.4	3.0	0.0	6.5	0.0	13.0	12.9	12.5	8.0	5.1	6.8	14.4	13.5	10.2	16.3	4.0	17.1
237	25.0	14.6	14.3	10.0	6.7	19.7	8.1	14.1	23.8	10.9	6.5	21.6	16.0	15.4	25.7	11.1	17.7	19.4	11.3	37.0	7.3
241	14.7	7.3	10.2	0.0	8.9	9.1	32.3	15.2	9.5	19.6	6.5	12.5	20.0	15.4	6.8	7.8	5.2	9.2	20.0	26.0	23.2
245	12.1	1.0	2.0	0.0	10.0	1.5	0.0	4.3	0.0	4.3	24.2	2.3	6.0	3.8	6.8	1.1	4.2	5.1	0.0	0.0	3.7
249	1.7	5.2	5.1	2.2	1.1	3.0	16.1	6.5	0.0	0.0	4.8	3.4	0.0	2.6	6.8	4.4	0.0	3.1	0.0	0.0	1.2
253	2.6	2.1	4.1	12.2	0.0	1.5	11.3	2.2	2.4	0.0	0.0	0.0	0.0	0.0	1.4	4.4	2.1	3.1	0.0	0.0	0.0
257	0.0	4.2	0.0	18.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.7	0.0	0.0	2.0	1.3	0.0	0.0
261	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	8.9	0.0	0.0	1.3	0.0	0.0
265	0.0	3.1	0.0	4.4	0.0	0.0	14.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	0.0	2.5	1.0	0.0
269	0.0	0.0	0.0	0.0	0.0	0.0	1.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
277	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Locus/ Alleles	Populations																					
Ema-D12a	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
181	0.0	0.0	4.5	1.0	0.0	0.0	1.0	2.6	3.8	1.1	3.0	0.0	4.4	0.0	0.0	0.0	0.0	0.9	2.4	0.0	6.1	4.5
185	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
193	0.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0	3.2	0.0	1.0	2.9	0.0	0.0	1.5	3.7	0.0	0.0	1.8	0.0	0.0
197	3.1	0.0	0.0	6.0	0.0	6.3	5.0	2.6	5.1	9.6	2.0	3.1	1.5	4.3	4.3	0.0	2.4	1.9	0.0	4.5	1.8	2.3
201	17.3	29.0	9.1	15.0	31.5	10.0	18.0	23.7	14.1	14.9	25.0	18.8	16.2	27.1	52.2	30.3	7.3	11.3	11.9	10.7	14.9	20.5
205	46.9	14.5	45.5	19.0	9.3	5.0	19.0	13.2	21.8	21.3	33.0	19.8	20.6	17.1	13.0	25.8	12.2	19.8	40.5	27.7	22.8	12.5
209	11.2	4.8	4.5	14.0	9.3	8.8	14.0	23.7	26.9	11.7	18.0	17.7	8.8	11.4	2.2	7.6	28.0	23.6	11.9	16.1	16.7	14.8
213	16.3	29.0	18.2	27.0	33.3	48.8	17.0	23.7	20.5	19.1	13.0	26.0	13.2	34.3	10.9	22.7	24.4	21.7	21.4	25.0	25.4	27.3
217	1.0	22.6	15.9	15.0	14.8	21.3	25.0	5.3	7.7	16.0	3.0	7.3	22.1	5.7	10.9	9.1	17.1	17.0	7.1	11.6	10.5	13.6
221	1.0	0.0	2.3	2.0	1.9	0.0	0.0	5.3	0.0	2.1	3.0	6.3	10.3	0.0	6.5	1.5	4.9	3.8	4.8	2.7	1.8	3.4
225	3.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0
229	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-D12a	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
181	0.8	0.0	0.0	0.0	0.0	0.0	0.0	6.5	0.0	0.0	0.0	1.3	4.2	3.9	2.6	0.0	1.1	6.1	1.3	0.0	0.0
185	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2
193	0.8	1.1	0.0	0.0	0.0	0.0	0.0	1.1	0.0	0.0	1.6	0.0	2.1	2.6	0.0	0.0	0.0	0.0	0.0	0.0	2.4
197	0.8	0.0	1.0	0.0	17.4	1.5	0.0	2.2	0.0	1.1	0.0	3.8	6.3	5.3	0.0	2.2	1.1	0.0	0.0	12.2	3.7
201	30.5	16.0	9.0	22.3	19.8	13.2	40.3	16.3	13.6	22.8	8.1	15.4	22.9	9.2	6.4	19.6	13.8	17.3	28.9	16.3	13.4
205	30.5	21.3	37.0	10.6	23.3	27.9	6.5	19.6	50.0	18.5	9.7	19.2	22.9	32.9	21.8	19.6	30.9	25.5	17.1	14.3	19.5
209	8.5	23.4	18.0	27.7	7.0	23.5	4.8	9.8	2.3	7.6	24.2	17.9	12.5	10.5	35.9	12.0	17.0	12.2	13.2	6.1	14.6
213	12.7	26.6	23.0	34.0	27.9	20.6	46.8	25.0	20.5	21.7	51.6	23.1	16.7	25.0	28.2	42.4	23.4	29.6	23.7	38.8	23.2
217	11.9	7.4	12.0	3.2	4.7	13.2	1.6	14.1	11.4	20.7	4.8	10.3	10.4	9.2	5.1	3.3	11.7	9.2	13.2	10.2	19.5
221	3.4	4.3	0.0	2.1	0.0	0.0	0.0	4.3	2.3	5.4	0.0	7.7	2.1	1.3	0.0	1.1	1.1	0.0	2.6	2.0	2.4
225	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	0.0	0.0	0.0	1.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
229	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Locus/ Alleles	Populations																					
Ema-D114	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
270	5.2	1.6	0.0	2.0	1.9	0.0	3.1	11.4	0.0	5.4	1.0	1.0	1.4	2.8	6.5	1.5	1.2	0.9	0.0	2.8	6.3	1.1
274	43.8	43.5	54.5	37.0	29.6	38.8	55.2	45.5	55.3	43.5	52.0	51.0	45.7	11.1	17.4	62.1	39.0	36.1	47.6	56.5	42.9	43.6
278	18.8	4.8	18.2	24.0	16.7	10.0	19.8	2.3	10.5	17.4	14.0	10.4	22.9	40.3	23.9	15.2	34.1	24.1	14.3	20.4	20.5	27.7
282	26.0	46.8	18.2	29.0	48.1	11.3	10.4	29.5	31.6	26.1	23.0	27.1	17.1	31.9	50.0	18.2	20.7	31.5	23.8	14.8	23.2	17.0
286	4.2	0.0	0.0	4.0	0.0	23.8	4.2	0.0	2.6	2.2	0.0	5.2	1.4	0.0	0.0	1.5	4.9	4.6	4.8	3.7	4.5	3.2
290	1.0	0.0	6.8	3.0	0.0	5.0	2.1	6.8	0.0	1.1	5.0	3.1	0.0	13.9	0.0	0.0	0.0	2.8	9.5	0.9	1.8	5.3
294	1.0	3.2	2.3	1.0	0.0	11.3	2.1	4.5	0.0	4.3	5.0	2.1	8.6	0.0	0.0	1.5	0.0	0.0	0.0	0.9	0.9	1.1
298	0.0	0.0	0.0	0.0	3.7	0.0	3.1	0.0	0.0	0.0	0.0	0.0	1.4	0.0	2.2	0.0	0.0	0.0	0.0	0.0	0.0	1.1
302	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-D114	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
270	1.9	2.1	2.2	10.6	2.4	1.5	0.0	2.2	0.0	3.3	10.0	1.4	6.0	0.0	1.4	0.0	5.6	2.0	2.6	0.0	3.7
274	38.0	36.2	71.1	37.2	61.9	55.9	28.3	51.1	54.5	42.2	40.0	45.9	44.0	50.0	23.0	27.2	46.7	58.2	57.7	46.0	40.2
278	15.7	10.6	13.3	21.3	14.3	17.6	13.3	16.3	0.0	36.7	30.0	16.2	16.0	10.3	25.7	21.7	8.9	12.2	10.3	28.0	18.3
282	42.6	36.2	8.9	21.3	13.1	22.1	51.7	22.8	45.5	8.9	16.7	20.3	28.0	34.6	35.1	26.1	26.7	19.4	24.4	24.0	31.7
286	0.0	4.3	0.0	6.4	1.2	2.9	0.0	1.1	0.0	0.0	3.3	12.2	0.0	0.0	5.4	2.2	3.3	2.0	1.3	0.0	3.7
290	1.9	7.4	4.4	3.2	2.4	0.0	6.7	3.3	0.0	8.9	0.0	2.7	4.0	2.6	5.4	22.8	3.3	5.1	3.8	1.0	1.2
294	0.0	2.1	0.0	0.0	4.8	0.0	0.0	3.3	0.0	0.0	0.0	1.4	0.0	2.6	0.0	0.0	5.6	1.0	0.0	1.0	1.2
298	0.0	1.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	0.0	4.1	0.0	0.0	0.0	0.0	0.0	0.0
302	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Locus/ Alleles	Populations																					
Ema-D116	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
239	0.0	0.0	0.0	2.0	0.0	0.0	2.1	0.0	2.4	3.2	1.0	1.0	0.0	0.0	2.2	0.0	3.7	0.0	0.0	3.7	3.6	1.0
243	12.0	0.0	18.2	0.0	0.0	0.0	3.1	2.5	3.6	3.2	6.0	5.2	5.7	0.0	0.0	1.5	0.0	3.4	9.5	7.4	6.3	1.0
247	20.0	58.1	47.7	23.0	25.9	23.8	22.9	27.5	28.6	28.7	26.0	37.5	32.9	22.2	23.9	39.4	34.1	27.6	16.7	22.2	26.8	26.0
251	27.0	1.6	13.6	26.0	9.3	6.3	18.8	5.0	23.8	19.1	29.0	8.3	12.9	20.8	15.2	18.2	11.0	31.0	38.1	23.1	20.5	27.1
255	12.0	1.6	6.8	12.0	9.3	5.0	12.5	2.5	3.6	12.8	4.0	13.5	14.3	2.8	13.0	6.1	11.0	7.8	9.5	13.0	8.0	11.5
259	1.0	6.5	2.3	15.0	9.3	6.3	16.7	2.5	4.8	8.5	6.0	2.1	8.6	11.1	17.4	1.5	13.4	11.2	0.0	0.9	6.3	7.3
263	0.0	6.5	0.0	3.0	11.1	41.3	4.2	5.0	0.0	3.2	0.0	3.1	0.0	5.6	28.3	7.6	2.4	1.7	0.0	2.8	2.7	3.1
267	7.0	4.8	2.3	6.0	3.7	6.3	6.3	2.5	4.8	9.6	7.0	2.1	2.9	30.6	0.0	19.7	12.2	3.4	4.8	4.6	5.4	9.4
271	7.0	0.0	6.8	3.0	1.9	8.8	3.1	27.5	9.5	3.2	5.0	14.6	7.1	6.9	0.0	0.0	0.0	0.9	7.1	10.2	7.1	2.1
275	7.0	9.7	0.0	4.0	7.4	0.0	2.1	0.0	3.6	4.3	5.0	4.2	2.9	0.0	0.0	1.5	6.1	8.6	4.8	3.7	4.5	4.2
279	6.0	11.3	2.3	4.0	16.7	2.5	7.3	25.0	15.5	3.2	8.0	7.3	12.9	0.0	0.0	4.5	3.7	0.0	4.8	7.4	4.5	5.2
283	1.0	0.0	0.0	1.0	5.6	0.0	1.0	0.0	0.0	1.1	2.0	0.0	0.0	0.0	0.0	0.0	2.4	3.4	0.0	0.0	0.0	2.1
287	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.0	0.9	3.6	0.0
291	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	4.8	0.0	0.0	0.0
295	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.0

Appendix 1. (Continued).

Locus/ Alleles	Populations																				
Ema-D116	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
239	0.0	0.0	2.0	0.0	3.6	0.0	0.0	0.0	0.0	0.0	0.0	3.4	0.0	1.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
243	0.9	1.0	0.0	1.2	0.0	5.9	0.0	1.1	4.8	0.0	0.0	1.1	8.3	5.1	1.3	0.0	1.0	1.0	11.3	6.1	3.7
247	35.2	21.9	14.0	24.4	21.4	32.4	54.8	27.2	28.6	20.7	32.3	25.0	29.2	32.1	15.8	19.6	22.9	33.7	18.8	42.9	28.0
251	4.6	3.1	41.0	3.5	42.9	17.6	25.8	17.4	35.7	22.8	21.0	22.7	20.8	20.5	9.2	10.9	26.0	18.4	11.3	4.1	20.7
255	9.3	1.0	6.0	2.3	6.0	16.2	6.5	9.8	0.0	12.0	6.5	15.9	16.7	15.4	11.8	17.4	7.3	10.2	8.8	19.4	6.1
259	13.9	0.0	5.0	7.0	14.3	7.4	0.0	5.4	0.0	25.0	12.9	8.0	0.0	7.7	3.9	0.0	7.3	3.1	10.0	7.1	9.8
263	17.6	1.0	10.0	17.4	0.0	2.9	0.0	3.3	0.0	1.1	0.0	0.0	0.0	0.0	3.9	0.0	4.2	1.0	0.0	5.1	4.9
267	7.4	27.1	13.0	7.0	8.3	4.4	0.0	5.4	11.9	15.2	27.4	10.2	12.5	2.6	11.8	31.5	7.3	6.1	11.3	2.0	11.0
271	2.8	26.0	7.0	26.7	0.0	0.0	8.1	4.3	19.0	0.0	0.0	4.5	6.3	2.6	11.8	10.9	13.5	3.1	15.0	6.1	2.4
275	0.0	7.3	2.0	0.0	0.0	4.4	0.0	15.2	0.0	3.3	0.0	1.1	2.1	2.6	21.1	4.3	4.2	8.2	7.5	0.0	8.5
279	3.7	9.4	0.0	1.2	2.4	5.9	4.8	2.2	0.0	0.0	0.0	3.4	2.1	3.8	5.3	5.4	4.2	9.2	1.3	6.1	2.4
283	1.9	1.0	0.0	0.0	0.0	1.5	0.0	2.2	0.0	0.0	0.0	1.1	2.1	3.8	1.3	0.0	2.1	0.0	1.3	1.0	1.2
287	2.8	0.0	0.0	2.3	1.2	1.5	0.0	6.5	0.0	0.0	0.0	3.4	0.0	1.3	1.3	0.0	0.0	5.1	1.3	0.0	1.2
291	0.0	1.0	0.0	7.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	0.0	0.0	0.0	1.0	2.5	0.0	0.0
295	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	0.0	0.0	0.0	0.0	0.0	0.0

Locus/ Alleles	Populations																				
Ema-D4	AM	AR	BA	BAV	BC	BI	BIG	BL	BN	CF	DAY	EC	GR	HA	HH	KA	KT	LAV	LC	LCO	LL	LSG
196	30.0	39.7	11.4	28.0	27.8	13.8	33.7	4.5	19.0	19.1	25.0	21.9	31.4	30.6	2.2	37.1	40.2	34.5	28.6	24.5	28.1	20.2
200	16.0	39.7	25.0	34.0	20.4	20.0	25.5	22.7	38.1	24.5	22.0	21.9	20.0	5.6	23.9	12.9	17.1	28.4	26.2	28.2	19.3	33.3
204	54.0	20.7	63.6	38.0	51.9	66.3	40.8	72.7	42.9	56.4	53.0	56.3	48.6	63.9	73.9	50.0	42.7	37.1	45.2	47.3	52.6	46.4

Locus/ Alleles	Populations																				
Ema-D4	MC	MCL	MN	MOS	NN	NT	PI	PM	POT	SI	SM	SOM	SPI	SQ	SS	TCF	TEA	TH	WCF	WO	WSL
196	51.7	21.4	13.0	31.5	43.3	20.6	24.2	21.7	9.1	40.2	45.0	13.6	26.0	25.7	3.8	23.9	28.1	19.4	22.5	17.0	30.5
200	15.5	20.4	24.0	22.8	27.8	26.5	32.3	26.1	34.1	30.4	35.0	25.0	20.0	14.9	33.3	8.7	26.0	28.6	37.5	33.0	23.2
204	32.8	58.2	63.0	45.7	28.9	52.9	43.5	52.2	56.8	29.3	20.0	61.4	54.0	59.5	62.8	67.4	45.8	52.0	40.0	50.0	46.3

Appendix 2. Muskellunge stocking records for all populations. Source is provided when possible. Ages are coded as follows: FI=Fingerling, FY=Fry, LF=Large Fingerling, YG=Yearling, SF=Small Fingerling. Population codes are given in Table 1.

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
AM	1972	UNSPECIFIED	FI	415	DNR COOP PONDS
	1973	UNSPECIFIED	FI	423	DNR HATCHERY
	1974	UNSPECIFIED	FI	856	DNR COOP PONDS
	1975	UNSPECIFIED	FI	303	DNR COOP PONDS
	1976	UNSPECIFIED	FI	2115	DNR COOP PONDS
	1977	UNSPECIFIED	FI	425	DNR COOP PONDS
	1978	UNSPECIFIED	FI	200	DNR HATCHERY
	1979	UNSPECIFIED	FI	425	DNR COOP PONDS
	1980	UNSPECIFIED	FI	425	DNR COOP PONDS
	1983	UNSPECIFIED	FI	400	DNR COOP PONDS
	1985	UNSPECIFIED	FI	400	DNR COOP PONDS
	1986	UNSPECIFIED	FI	400	DNR COOP PONDS
	1987	UNSPECIFIED	FI	600	DNR HATCHERY
	1988	UNSPECIFIED	FI	400	DNR HATCHERY
	1989	UNSPECIFIED	FI	200	DNR HATCHERY
	1990	UNSPECIFIED	FI	200	DNR HATCHERY
	1991	UNSPECIFIED	FI	400	DNR HATCHERY
	1992	UNSPECIFIED	FI	400	DNR HATCHERY
	1993	UNSPECIFIED	FI	400	DNR HATCHERY
	1996	UNSPECIFIED	FI	1600	DNR HATCHERY
	1997	UNSPECIFIED	LF	200	DNR HATCHERY
	2005	UNSPECIFIED	LF	100	PRIVATE HATCHERY
BA	1984	UNSPECIFIED	FY	188000	DNR HATCHERY
BAV	1972	UNSPECIFIED	FI	2100	DNR COOP PONDS
	1973	UNSPECIFIED	FI	1198	DNR COOP PONDS
	1974	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1974	UNSPECIFIED	FI	200	DNR HATCHERY
	1977	UNSPECIFIED	FI	1939	DNR COOP PONDS
	1979	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1980	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1981	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1982	UNSPECIFIED	FY	85050	DNR HATCHERY
	1983	UNSPECIFIED	FI	2084	DNR COOP PONDS
	1985	UNSPECIFIED	FY	82400	DNR HATCHERY
	1986	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1988	UNSPECIFIED	FI	1211	DNR HATCHERY
	1989	UNSPECIFIED	FI	2720	DNR HATCHERY
	1990	UNSPECIFIED	FI	232	DNR COOP PONDS
	1990	UNSPECIFIED	FI	768	DNR HATCHERY
	1991	UNSPECIFIED	FI	383	DNR COOP PONDS
	1991	UNSPECIFIED	FI	167	DNR HATCHERY
	1991	UNSPECIFIED	FY	180703	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
BAV	1992	UNSPECIFIED	FI	91	DNR HATCHERY
	1992	UNSPECIFIED	FY	95500	DNR HATCHERY
	1993	UNSPECIFIED	FY	148400	DNR HATCHERY
	1994	UNSPECIFIED	FY	60000	DNR HATCHERY
	1995	UNSPECIFIED	FY	163900	DNR HATCHERY
	1996	UNSPECIFIED	FI	944	DNR HATCHERY
	1996	UNSPECIFIED	FY	201900	DNR HATCHERY
	1998	UNSPECIFIED	FY	100000	DNR HATCHERY
	1998	UNSPECIFIED	LF	1167	DNR HATCHERY
	1999	UNSPECIFIED	FY	220300	DNR HATCHERY
	2000	UNSPECIFIED	FY	136350	DNR HATCHERY
	2000	UNSPECIFIED	LF	1100	DNR HATCHERY
	2000	UNSPECIFIED	SF	11688	DNR HATCHERY
	2001	UNSPECIFIED	FY	345200	DNR HATCHERY
	2002	UNSPECIFIED	LF	1090	DNR HATCHERY
	2004	UNSPECIFIED	LF	1090	DNR HATCHERY
	2006	UPPER WISCONSIN RIVER	LF	703	DNR HATCHERY
	2008	UPPER WISCONSIN RIVER	LF	1090	DNR HATCHERY
BC	1975	UNSPECIFIED	FY	50000	PRIVATE HATCHERY
BIG	1973	UNSPECIFIED	FI	1900	DNR COOP PONDS
	1976	UNSPECIFIED	FI	600	DNR COOP PONDS
	1977	UNSPECIFIED	FI	1005	DNR COOP PONDS
	1980	UNSPECIFIED	FI	1712	DNR COOP PONDS
	1983	UNSPECIFIED	FI	1700	DNR COOP PONDS
	1985	UNSPECIFIED	FI	4	FIELD TRANSFER
	1986	UNSPECIFIED	FI	1700	DNR COOP PONDS
	1988	UNSPECIFIED	FI	1700	DNR HATCHERY
	1990	UNSPECIFIED	FI	1700	DNR HATCHERY
	1991	UNSPECIFIED	FI	800	DNR HATCHERY
	1995	UNSPECIFIED	FY	25000	DNR HATCHERY
	2000	UNSPECIFIED	FY	103350	DNR HATCHERY
	2001	UNSPECIFIED	FY	172800	DNR HATCHERY
BI	1980	UNSPECIFIED	FI	1000	DNR COOP PONDS
BL	1986-1992*				
BN	1972	UNSPECIFIED	FI	500	DNR COOP PONDS
	1973	UNSPECIFIED	FI	400	DNR HATCHERY
	1974	UNSPECIFIED	FI	2009	DNR COOP PONDS
	1975	UNSPECIFIED	FI	651	DNR COOP PONDS
	1976	UNSPECIFIED	FI	3000	DNR COOP PONDS
	1977	UNSPECIFIED	FI	1300	DNR COOP PONDS
	1977	UNSPECIFIED	FI	1200	DNR HATCHERY
	1978	UNSPECIFIED	FI	1733	DNR COOP PONDS

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
BN	1979	UNSPECIFIED	FI	4444	DNR COOP PONDS
	1980	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1981	UNSPECIFIED	FI	500	DNR COOP PONDS
	1982	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1983	UNSPECIFIED	FI	1512	DNR COOP PONDS
	1984	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1985	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1986	UNSPECIFIED	FI	2000	DNR HATCHERY
	1987	UNSPECIFIED	FI	3000	DNR HATCHERY
	1988	UNSPECIFIED	FI	2000	DNR HATCHERY
	1989	UNSPECIFIED	FI	1000	DNR HATCHERY
	1990	UNSPECIFIED	FI	1000	DNR HATCHERY
	1991	UNSPECIFIED	FI	2000	DNR HATCHERY
	1993	UNSPECIFIED	FI	2000	DNR HATCHERY
	1995	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1999	UNSPECIFIED	LF	500	DNR HATCHERY
CF	1974	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1975	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1976	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1977	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1978	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1979	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1980	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1982	UNSPECIFIED	FI	835	DNR COOP PONDS
	1983	UNSPECIFIED	FI	2227	DNR COOP PONDS
	1986	UNSPECIFIED	FY	1000	DNR COOP PONDS
	1987	UNSPECIFIED	FI	3000	DNR COOP PONDS
	1988	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1989	UNSPECIFIED	FI	1000	DNR HATCHERY
	1990	UNSPECIFIED	FI	1000	DNR HATCHERY
	1991	UNSPECIFIED	FI	747	DNR HATCHERY
	1992	UNSPECIFIED	FI	1000	DNR HATCHERY
	1993	UNSPECIFIED	FI	274	DNR HATCHERY
	1993	UNSPECIFIED	FI	730	DNR COOP PONDS
	1995	UNSPECIFIED	FI	908	DNR HATCHERY
	1996	UNSPECIFIED	FI	500	DNR HATCHERY
	1999	UNSPECIFIED	LF	1000	DNR HATCHERY
	2000	UNSPECIFIED	LF	850	DNR HATCHERY
	2001	UNSPECIFIED	LF	1000	DNR HATCHERY
	2002	UNSPECIFIED	LF	998	DNR HATCHERY
	2003	UNSPECIFIED	LF	1000	DNR HATCHERY
	2004	UNSPECIFIED	LF	999	DNR HATCHERY
	2005	UNSPECIFIED	LF	999	DNR HATCHERY
	2006	UPPER WISCONSIN RIVER	LF	219	DNR HATCHERY
	2007	UPPER CHIPPEWA RIVER	LF	667	DNR HATCHERY
	2008	UPPER WISCONSIN RIVER	LF	997	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
MCL	1979	UNSPECIFIED	FI	150	DNR COOP PONDS
	1982	UNSPECIFIED	FI	2000	DNR COOP PONDS
DAY	1972	UNSPECIFIED	FI	423	DNR COOP PONDS
	1973	UNSPECIFIED	FI	600	DNR HATCHERY
	1974	UNSPECIFIED	FI	1250	DNR COOP PONDS
	1975	UNSPECIFIED	FI	128	DNR COOP PONDS
	1976	UNSPECIFIED	FI	1900	DNR COOP PONDS
	1977	UNSPECIFIED	FI	682	DNR HATCHERY
	1977	UNSPECIFIED	FI	600	DNR COOP PONDS
	1978	UNSPECIFIED	FI	636	DNR HATCHERY
	1980	UNSPECIFIED	FI	640	DNR COOP PONDS
	1982	UNSPECIFIED	FI	320	DNR COOP PONDS
	1984	UNSPECIFIED	FI	640	DNR COOP PONDS
	1986	UNSPECIFIED	FI	1280	DNR COOP PONDS
	1988	UNSPECIFIED	FI	1280	DNR HATCHERY
	1990	UNSPECIFIED	FI	1280	DNR HATCHERY
EC/WCF	1972	UNSPECIFIED	FI	732	DNR COOP PONDS
	1973	UNSPECIFIED	FI	210	DNR HATCHERY
	1976	UNSPECIFIED	FI	700	DNR COOP PONDS
	1977	UNSPECIFIED	FI	600	DNR COOP PONDS
	1979	UNSPECIFIED	FI	550	DNR COOP PONDS
	1983	UNSPECIFIED	FI	400	DNR COOP PONDS
	1985	UNSPECIFIED	FI	900	DNR COOP PONDS
	1987	UNSPECIFIED	FI	2700	DNR HATCHERY
	1988	UNSPECIFIED	FI	500	DNR HATCHERY
	1989	UNSPECIFIED	FI	900	DNR HATCHERY
	1990	UNSPECIFIED	FI	900	DNR HATCHERY
	1991	UNSPECIFIED	FI	900	DNR HATCHERY
	1992	UNSPECIFIED	FI	1172	DNR HATCHERY
	1993	UNSPECIFIED	FI	1172	DNR HATCHERY
	1996	UNSPECIFIED	FI	1172	DNR HATCHERY
	1997	UNSPECIFIED	LF	225	DNR HATCHERY
	2000	UNSPECIFIED	LF	1124	DNR HATCHERY
	2002	UNSPECIFIED	LF	1134	DNR HATCHERY
	2004	UNSPECIFIED	LF	841	DNR HATCHERY
	2006	UPPER CHIPPEWA RIVER	LF	161	DNR HATCHERY
	2008	UPPER CHIPPEWA RIVER	LF	293	DNR HATCHERY
GR	1972	UNSPECIFIED	FI	1650	DNR COOP PONDS
	1973	UNSPECIFIED	FI	600	DNR HATCHERY
	1975	UNSPECIFIED	FI	986	DNR COOP PONDS
	1976	UNSPECIFIED	FI	2802	DNR COOP PONDS
	1977	UNSPECIFIED	FI	3500	DNR HATCHERY
	1978	UNSPECIFIED	FI	3500	DNR HATCHERY
	1979	UNSPECIFIED	FI	2748	DNR COOP PONDS

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
GR	1980	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1981	UNSPECIFIED	FI	700	DNR COOP PONDS
	1982	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1983	UNSPECIFIED	FI	1250	DNR COOP PONDS
	1984	UNSPECIFIED	FI	1300	DNR COOP PONDS
	1985	UNSPECIFIED	FI	490	FIELD TRANSFER
	1985	UNSPECIFIED	FI	4000	DNR COOP PONDS
	1986	UNSPECIFIED	FI	1732	DNR COOP PONDS
	1986	UNSPECIFIED	FI	268	DNR HATCHERY
	1987	UNSPECIFIED	FI	3000	DNR HATCHERY
	1988	UNSPECIFIED	FI	4510	DNR HATCHERY
	1989	UNSPECIFIED	FI	1000	DNR HATCHERY
	1990	UNSPECIFIED	FI	1000	DNR HATCHERY
	1991	UNSPECIFIED	FI	3300	DNR HATCHERY
	1992	UNSPECIFIED	FI	1500	DNR HATCHERY
	1993	UNSPECIFIED	FI	1500	DNR HATCHERY
	1996	UNSPECIFIED	FI	1501	DNR HATCHERY
	1997	UNSPECIFIED	LF	750	DNR HATCHERY
	2000	UNSPECIFIED	LF	1500	DNR HATCHERY
	2001	UNSPECIFIED	LF	3011	DNR HATCHERY
	2003	UNSPECIFIED	LF	2499	DNR HATCHERY
	2005	UPPER CHIPPEWA RIVER	LF	1881	DNR HATCHERY
	2007	UPPER CHIPPEWA RIVER	LF	1755	DNR HATCHERY
HA	1978	UNSPECIFIED	FI	1020	DNR COOP PONDS
HH	NO RECORDED STOCKING EVENTS BETWEEN 1972 – 2008				
KA	1982	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1993	UNSPECIFIED	FY	117300	DNR HATCHERY
	1994	UNSPECIFIED	FY	25000	DNR HATCHERY
	1995	UNSPECIFIED	FY	162000	DNR HATCHERY
	1998	UNSPECIFIED	FY	56000	DNR HATCHERY
	1999	UNSPECIFIED	FY	18900	DNR HATCHERY
KT	1981	UNSPECIFIED	FI	150	FIELD TRANSFER
	NR				
LCO	1972	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1972	UNSPECIFIED	FY	242600	DNR HATCHERY
	1973	UNSPECIFIED	FI	500	DNR HATCHERY
	1973	UNSPECIFIED	FY	243000	DNR HATCHERY
	1974	UNSPECIFIED	FI	94	DNR COOP PONDS
	1974	UNSPECIFIED	FY	315000	DNR HATCHERY
	1975	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1975	UNSPECIFIED	FY	102600	DNR HATCHERY
	1976	UNSPECIFIED	FI	4000	DNR COOP PONDS

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
LCO	1976	UNSPECIFIED	FY	250000	DNR HATCHERY
	1977	UNSPECIFIED	FI	1320	DNR COOP PONDS
	1977	UNSPECIFIED	FI	1500	DNR HATCHERY
	1977	UNSPECIFIED	FY	78300	DNR HATCHERY
	1978	UNSPECIFIED	FI	500	DNR COOP PONDS
	1978	UNSPECIFIED	FI	1000	DNR HATCHERY
	1978	UNSPECIFIED	FY	105300	DNR HATCHERY
	1979	UNSPECIFIED	FI	3807	DNR COOP PONDS
	1979	UNSPECIFIED	FY	574695	DNR HATCHERY
	1980	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1980	UNSPECIFIED	FY	261400	DNR HATCHERY
	1981	UNSPECIFIED	FI	820	DNR COOP PONDS
	1981	UNSPECIFIED	FY	322761	DNR HATCHERY
	1982	UNSPECIFIED	FI	1360	DNR COOP PONDS
	1982	UNSPECIFIED	FY	442125	DNR HATCHERY
	1983	UNSPECIFIED	FI	1250	DNR COOP PONDS
	1983	UNSPECIFIED	FY	194400	DNR HATCHERY
	1984	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1984	UNSPECIFIED	FY	548500	DNR HATCHERY
	1985	UNSPECIFIED	FI	5237	DNR COOP PONDS
	1985	UNSPECIFIED	FY	414684	DNR HATCHERY
	1986	UNSPECIFIED	FI	1188	DNR COOP PONDS
	1986	UNSPECIFIED	FI	812	DNR HATCHERY
	1986	UNSPECIFIED	FY	100000	DNR HATCHERY
	1987	UNSPECIFIED	FI	5595	DNR HATCHERY
	1987	UNSPECIFIED	FY	278280	DNR HATCHERY
	1988	UNSPECIFIED	FI	5000	DNR HATCHERY
	1988	UNSPECIFIED	FY	150000	DNR HATCHERY
	1989	UNSPECIFIED	FI	1533	DNR HATCHERY
	1989	UNSPECIFIED	FY	200000	DNR HATCHERY
	1989	UNSPECIFIED	YG	155	DNR HATCHERY
	1990	UNSPECIFIED	FI	1250	DNR HATCHERY
	1990	UNSPECIFIED	FY	60000	DNR HATCHERY
	1991	UNSPECIFIED	FI	3000	DNR HATCHERY
	1991	UNSPECIFIED	FY	396900	DNR HATCHERY
	1992	UNSPECIFIED	FI	2500	DNR HATCHERY
	1992	UNSPECIFIED	FY	300000	DNR HATCHERY
	1993	UNSPECIFIED	FI	2510	DNR HATCHERY
	1993	UNSPECIFIED	FY	52000	DNR HATCHERY
	1996	UNSPECIFIED	FI	1500	DNR HATCHERY
	1996	UNSPECIFIED	FY	424000	DNR HATCHERY
	1997	UNSPECIFIED	FY	440000	DNR HATCHERY
	1997	UNSPECIFIED	LF	750	DNR HATCHERY
	1998	UNSPECIFIED	FY	200000	DNR HATCHERY
	1998	UNSPECIFIED	LF	1500	DNR HATCHERY
	1999	UNSPECIFIED	FY	75000	DNR HATCHERY
	2000	UNSPECIFIED	LF	1500	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
LCO	2001	UNSPECIFIED	FY	60000	DNR HATCHERY
	2001	UNSPECIFIED	LF	2519	DNR HATCHERY
	2003	UNSPECIFIED	LF	2493	DNR HATCHERY
	2005	UPPER CHIPPEWA RIVER	LF	1882	DNR HATCHERY
	2007	UPPER CHIPPEWA RIVER	LF	2496	DNR HATCHERY
LAV	1972	UNSPECIFIED	FI	1200	DNR COOP PONDS
	1973	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1974	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1975	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1976	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1977	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1979	UNSPECIFIED	FI	500	DNR COOP PONDS
	1980	UNSPECIFIED	FI	1179	DNR COOP PONDS
	1981	UNSPECIFIED	FI	400	DNR COOP PONDS
	1982	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1983	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1984	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1985	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1986	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1986	UNSPECIFIED	FY	67500	DNR HATCHERY
	1987	UNSPECIFIED	FI	2218	DNR COOP PONDS
	1987	UNSPECIFIED	FI	1109	DNR HATCHERY
	1987	UNSPECIFIED	FY	33000	DNR HATCHERY
	1988	UNSPECIFIED	FI	1091	DNR HATCHERY
	1988	UNSPECIFIED	FY	40500	DNR HATCHERY
	1989	UNSPECIFIED	FI	3050	DNR HATCHERY
	1990	UNSPECIFIED	FY	32400	DNR HATCHERY
	1991	UNSPECIFIED	FI	500	DNR COOP PONDS
	1992	UNSPECIFIED	FI	500	DNR HATCHERY
	1993	UNSPECIFIED	FI	500	DNR COOP PONDS
	1993	UNSPECIFIED	FY	67300	DNR HATCHERY
	1996	UNSPECIFIED	FY	27000	DNR HATCHERY
	1997	UNSPECIFIED	FY	225000	DNR HATCHERY
	1998	UNSPECIFIED	FY	115000	DNR HATCHERY
	1998	UNSPECIFIED	LF	500	DNR HATCHERY
	1999	UNSPECIFIED	FY	379150	DNR HATCHERY
	2000	UNSPECIFIED	FY	161050	DNR HATCHERY
	2000	UNSPECIFIED	LF	500	DNR HATCHERY
	2000	UNSPECIFIED	SF	12927	DNR HATCHERY
	2001	UNSPECIFIED	FY	342850	DNR HATCHERY
	2001	UNSPECIFIED	LF	267	DNR HATCHERY
	2003	UNSPECIFIED	LF	266	DNR HATCHERY
	2005	UNSPECIFIED	LF	267	DNR HATCHERY
	2007	UPPER WISCONSIN RIVER	LF	178	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
LSG	1972	UNSPECIFIED	FI	1827	DNR COOP PONDS
	1973	UNSPECIFIED	FI	1119	DNR COOP PONDS
	1973	UNSPECIFIED	FY	35000	DNR HATCHERY
	1974	UNSPECIFIED	FI	642	DNR COOP PONDS
	1974	UNSPECIFIED	FI	600	DNR HATCHERY
	1976	UNSPECIFIED	FI	500	DNR COOP PONDS
	1979	UNSPECIFIED	FI	1876	DNR COOP PONDS
	1983	UNSPECIFIED	FI	1804	DNR COOP PONDS
	1984	UNSPECIFIED	FI	1916	DNR COOP PONDS
	1985	UNSPECIFIED	FI	2945	DNR COOP PONDS
	1986	UNSPECIFIED	FI	1409	DNR COOP PONDS
	1986	UNSPECIFIED	FI	800	DNR HATCHERY
	1987	UNSPECIFIED	FI	3796	DNR COOP PONDS
	1987	UNSPECIFIED	FI	1898	DNR HATCHERY
	1988	UNSPECIFIED	FI	2249	DNR HATCHERY
	1990	UNSPECIFIED	FI	1900	DNR HATCHERY
	1996	UNSPECIFIED	FI	2021	DNR HATCHERY
	1998	UNSPECIFIED	FY	80000	DNR HATCHERY
	1998	UNSPECIFIED	LF	1774	DNR HATCHERY
	2000	UNSPECIFIED	LF	1800	DNR HATCHERY
	2002	UNSPECIFIED	LF	490	DNR HATCHERY
	2004	UNSPECIFIED	LF	490	DNR HATCHERY
	2006	UPPER WISCONSIN RIVER	LF	490	DNR HATCHERY
	2008	UPPER WISCONSIN RIVER	LF	490	DNR HATCHERY
LL	1972	UNSPECIFIED	FI	800	DNR COOP PONDS
	1973	UNSPECIFIED	FI	401	DNR HATCHERY
	1975	UNSPECIFIED	FI	964	DNR COOP PONDS
	1976	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1977	UNSPECIFIED	FI	700	DNR COOP PONDS
	1977	UNSPECIFIED	FI	800	DNR HATCHERY
	1978	UNSPECIFIED	FI	1500	DNR HATCHERY
	1979	UNSPECIFIED	FI	2840	DNR COOP PONDS
	1980	UNSPECIFIED	FI	1500	DNR COOP PONDS
	1981	UNSPECIFIED	FI	400	DNR COOP PONDS
	1982	UNSPECIFIED	FI	735	DNR COOP PONDS
	1983	UNSPECIFIED	FI	1113	DNR COOP PONDS
	1984	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1985	UNSPECIFIED	FI	2564	DNR COOP PONDS
	1986	UNSPECIFIED	FI	1500	DNR HATCHERY
	1987	UNSPECIFIED	FI	2250	DNR HATCHERY
	1988	UNSPECIFIED	FI	1500	DNR HATCHERY
	1989	UNSPECIFIED	FI	805	DNR HATCHERY
	1990	UNSPECIFIED	FI	750	DNR HATCHERY
	1991	UNSPECIFIED	FI	1500	DNR HATCHERY
	1992	UNSPECIFIED	FI	1304	DNR HATCHERY
	1993	UNSPECIFIED	FI	1708	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
LL	1996	UNSPECIFIED	FI	1304	DNR HATCHERY
	1997	UNSPECIFIED	LF	326	DNR HATCHERY
	2000	UNSPECIFIED	LF	1304	DNR HATCHERY
	2001	UNSPECIFIED	LF	652	DNR HATCHERY
	2003	UNSPECIFIED	LF	652	DNR HATCHERY
	2005	UPPER CHIPPEWA RIVER	LF	522	DNR HATCHERY
	2007	UPPER CHIPPEWA RIVER	LF	435	DNR HATCHERY
LC	NR				
MN	1972	UNSPECIFIED	FI	225	DNR COOP PONDS
	1973	UNSPECIFIED	FI	200	DNR HATCHERY
	1974	UNSPECIFIED	FI	450	DNR COOP PONDS
	1975	UNSPECIFIED	FI	45	DNR COOP PONDS
	1976	UNSPECIFIED	FI	450	DNR COOP PONDS
MC	1972	UNSPECIFIED	FI	1050	DNR COOP PONDS
	1975	UNSPECIFIED	FI	500	DNR COOP PONDS
	1977	UNSPECIFIED	FI	900	DNR COOP PONDS
	1980	UNSPECIFIED	FI	470	DNR COOP PONDS
	1981	UNSPECIFIED	FI	500	DNR COOP PONDS
	1989	UNSPECIFIED	FI	400	DNR HATCHERY
MOS	NR				
NT	1972	UNSPECIFIED	FI	1604	DNR COOP PONDS
	1972	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1974	UNSPECIFIED	FI	2900	DNR COOP PONDS
	1974	UNSPECIFIED	FI	944	DNR COOP PONDS
	1976	UNSPECIFIED	FI	1184	DNR COOP PONDS
	1976	UNSPECIFIED	FI	848	DNR COOP PONDS
	1977	UNSPECIFIED	FI	14518	DNR COOP PONDS
	1977	UNSPECIFIED	FI	1717	DNR COOP PONDS
	1979	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1980	UNSPECIFIED	FI	300	FIELD TRANSFER
	1981	UNSPECIFIED	FI	993	DNR COOP PONDS
	1981	UNSPECIFIED	FI	600	DNR COOP PONDS
	1982	UNSPECIFIED	FI	2320	DNR COOP PONDS
	1984	UNSPECIFIED	FI	500	DNR COOP PONDS
	1985	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1985	UNSPECIFIED	FI	145	FIELD TRANSFER
	1986	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1986	UNSPECIFIED	FI	200	FIELD TRANSFER
	1986	UNSPECIFIED	FI	200	FIELD TRANSFER
	1987	UNSPECIFIED	FI	5000	DNR COOP PONDS
	1987	UNSPECIFIED	FI	2500	DNR HATCHERY
	1988	UNSPECIFIED	FI	2484	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
NT	1989	UNSPECIFIED	FI	2000	DNR HATCHERY
	1989	UNSPECIFIED	FY	10800	DNR HATCHERY
	1993	UNSPECIFIED	FY	37800	DNR HATCHERY
	1995	UNSPECIFIED	FY	80000	DNR HATCHERY
PI	1975	UNSPECIFIED	FI	62	DNR COOP PONDS
PM	1973	UNSPECIFIED	FI	1100	DNR COOP PONDS
	1974	UNSPECIFIED	FI	300	DNR COOP PONDS
	1977	UNSPECIFIED	FI	2536	DNR COOP PONDS
	1983	UNSPECIFIED	FI	1800	DNR COOP PONDS
	1985	UNSPECIFIED	FI	1800	DNR COOP PONDS
	1986	UNSPECIFIED	FI	508	DNR COOP PONDS
	1987	UNSPECIFIED	FI	3552	DNR COOP PONDS
	1987	UNSPECIFIED	FI	1776	DNR HATCHERY
	1989	UNSPECIFIED	FI	900	DNR HATCHERY
	1991	UNSPECIFIED	FI	60	DNR HATCHERY
	1991	UNSPECIFIED	FI	840	DNR COOP PONDS
	1992	UNSPECIFIED	FI	247	DNR COOP PONDS
	1992	UNSPECIFIED	FI	900	DNR HATCHERY
	1999	UNSPECIFIED	LF	847	DNR HATCHERY
POT	NR				
SI	1972	UNSPECIFIED	FI	275	DNR COOP PONDS
	1974	UNSPECIFIED	FI	340	DNR HATCHERY
	1976	UNSPECIFIED	FI	275	DNR COOP PONDS
	1979	UNSPECIFIED	FI	275	DNR COOP PONDS
SM	NR				
SOM	1991	UNSPECIFIED	FI	900	DNR HATCHERY
	1993	UNSPECIFIED	FI	944	DNR HATCHERY
	1995	UNSPECIFIED	FI	944	DNR HATCHERY
	1997	UNSPECIFIED	LF	340	DNR HATCHERY
	1999	UNSPECIFIED	LF	472	DNR HATCHERY
	2000	UNSPECIFIED	LF	472	DNR HATCHERY
	2001	UNSPECIFIED	LF	472	DNR HATCHERY
	2003	UNSPECIFIED	LF	472	DNR HATCHERY
	2005	UNSPECIFIED	LF	472	DNR HATCHERY
	2007	UPPER WISCONSIN RIVER	LF	315	DNR HATCHERY
SPI	1972	UNSPECIFIED	FI	350	DNR COOP PONDS
	1973	UNSPECIFIED	FI	300	DNR HATCHERY
	1974	UNSPECIFIED	FI	700	DNR COOP PONDS
	1975	UNSPECIFIED	FI	450	DNR COOP PONDS
	1976	UNSPECIFIED	FI	700	DNR COOP PONDS

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
SPI	1977	UNSPECIFIED	FI	722	DNR COOP PONDS
	1978	UNSPECIFIED	FI	495	DNR COOP PONDS
	1979	UNSPECIFIED	FI	720	DNR COOP PONDS
	1980	UNSPECIFIED	FI	720	DNR COOP PONDS
	1981	UNSPECIFIED	FI	300	DNR COOP PONDS
	1982	UNSPECIFIED	FI	360	DNR COOP PONDS
	1983	UNSPECIFIED	FI	720	DNR HATCHERY
	1984	UNSPECIFIED	FI	468	DNR COOP PONDS
	1985	UNSPECIFIED	FI	720	DNR COOP PONDS
	1986	UNSPECIFIED	FI	720	DNR COOP PONDS
	1987	UNSPECIFIED	FI	1080	DNR HATCHERY
	1988	UNSPECIFIED	FI	720	DNR HATCHERY
	1989	UNSPECIFIED	FI	360	DNR HATCHERY
	1990	UNSPECIFIED	FI	360	DNR HATCHERY
	1991	UNSPECIFIED	FI	720	DNR HATCHERY
	1992	UNSPECIFIED	FI	704	DNR HATCHERY
	1993	UNSPECIFIED	FI	704	DNR HATCHERY
	1995	UNSPECIFIED	FI	352	DNR HATCHERY
	1972	UNSPECIFIED	FI	800	DNR COOP PONDS
	1976	UNSPECIFIED	FI	2000	DNR COOP PONDS
	1977	UNSPECIFIED	FI	465	DNR HATCHERY
	1984	UNSPECIFIED	FI	200	DNR COOP PONDS
	1991	UNSPECIFIED	FI	200	PRIVATE HAT.
SQ	1972	UNSPECIFIED	FY	355637	DNR HATCHERY
	1973	UNSPECIFIED	FI	2815	DNR COOP PONDS
	1973	UNSPECIFIED	FY	130000	DNR HATCHERY
	1974	UNSPECIFIED	FI	1620	DNR COOP PONDS
	1974	UNSPECIFIED	FY	313200	DNR HATCHERY
	1975	UNSPECIFIED	FY	51300	DNR HATCHERY
	1976	UNSPECIFIED	FI	900	DNR COOP PONDS
	1976	UNSPECIFIED	FY	200000	DNR HATCHERY
	1977	UNSPECIFIED	FY	100000	DNR HATCHERY
	1979	UNSPECIFIED	FI	6558	DNR COOP PONDS
	1979	UNSPECIFIED	FY	35000	DNR HATCHERY
	1980	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1980	UNSPECIFIED	FY	125550	DNR HATCHERY
	1981	UNSPECIFIED	FI	1378	DNR COOP PONDS
	1981	UNSPECIFIED	FY	106650	DNR HATCHERY
	1982	UNSPECIFIED	FI	1050	DNR COOP PONDS
	1982	UNSPECIFIED	FY	188000	DNR HATCHERY
	1983	UNSPECIFIED	FI	1300	DNR COOP PONDS
	1983	UNSPECIFIED	FY	291600	DNR HATCHERY
	1984	UNSPECIFIED	FI	200	DNR COOP PONDS
	1984	UNSPECIFIED	FY	55350	DNR HATCHERY
	1985	UNSPECIFIED	FI	1314	DNR COOP PONDS
	1985	UNSPECIFIED	FY	35100	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
SQ	1986	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1986	UNSPECIFIED	FI	300	DNR HATCHERY
	1986	UNSPECIFIED	FY	67500	DNR HATCHERY
	1987	UNSPECIFIED	FI	2470	DNR COOP PONDS
	1987	UNSPECIFIED	FI	1235	DNR HATCHERY
	1988	UNSPECIFIED	FI	1300	DNR HATCHERY
	1989	UNSPECIFIED	FI	1295	DNR HATCHERY
	1989	UNSPECIFIED	FY	32400	DNR HATCHERY
	1990	UNSPECIFIED	FY	37800	DNR HATCHERY
	1991	UNSPECIFIED	FI	910	DNR COOP PONDS
	1991	UNSPECIFIED	FI	390	DNR HATCHERY
	1992	UNSPECIFIED	FI	1300	DNR HATCHERY
	1992	UNSPECIFIED	FY	46000	DNR HATCHERY
	1993	UNSPECIFIED	FI	1000	DNR COOP PONDS
	1993	UNSPECIFIED	FI	1500	DNR HATCHERY
	1995	UNSPECIFIED	FI	1280	DNR HATCHERY
	1996	UNSPECIFIED	FY	100000	DNR HATCHERY
	1997	UNSPECIFIED	FY	125000	DNR HATCHERY
	1997	UNSPECIFIED	LF	1520	DNR HATCHERY
	1998	UNSPECIFIED	FY	53000	DNR HATCHERY
	1999	UNSPECIFIED	FY	122950	DNR HATCHERY
	1999	UNSPECIFIED	LF	1000	DNR HATCHERY
	2000	UNSPECIFIED	FY	45900	DNR HATCHERY
	2001	UNSPECIFIED	FY	234000	DNR HATCHERY
	2001	UNSPECIFIED	LF	658	DNR HATCHERY
	2003	UNSPECIFIED	LF	648	DNR HATCHERY
	2005	UNSPECIFIED	LF	658	DNR HATCHERY
TEA	1972	UNSPECIFIED	FI	550	DNR COOP PONDS
	1973	UNSPECIFIED	FI	300	DNR HATCHERY
	1976	UNSPECIFIED	FI	1560	DNR COOP PONDS
	1977	UNSPECIFIED	FI	500	DNR COOP PONDS
	1977	UNSPECIFIED	FI	500	DNR HATCHERY
	1978	UNSPECIFIED	FI	1000	DNR HATCHERY
	1979	UNSPECIFIED	FI	2875	DNR COOP PONDS
	1980	UNSPECIFIED	FI	600	DNR COOP PONDS
	1981	UNSPECIFIED	FI	410	DNR COOP PONDS
	1982	UNSPECIFIED	FI	500	DNR COOP PONDS
	1983	UNSPECIFIED	FI	500	DNR COOP PONDS
	1984	UNSPECIFIED	FI	600	DNR COOP PONDS
	1985	UNSPECIFIED	FI	2100	DNR COOP PONDS
	1986	UNSPECIFIED	FI	900	DNR COOP PONDS
	1987	UNSPECIFIED	FI	1500	DNR HATCHERY
	1988	UNSPECIFIED	FI	1000	DNR HATCHERY
	1989	UNSPECIFIED	FI	500	DNR HATCHERY
	1990	UNSPECIFIED	FI	900	DNR HATCHERY
	1991	UNSPECIFIED	FI	1000	DNR HATCHERY

Appendix 2. (Continued).

Population	Year	Strain (Stock)	Age	# Stocked	Source Type
TEA	1991	UNSPECIFIED	FI	300	PRIVATE HAT.
	1992	UNSPECIFIED	FI	1049	DNR HATCHERY
	1993	UNSPECIFIED	FI	2000	DNR HATCHERY
	1996	UNSPECIFIED	FI	1024	DNR HATCHERY
	1997	UNSPECIFIED	LF	256	DNR HATCHERY
	2000	UNSPECIFIED	LF	1000	DNR HATCHERY
	2001	UNSPECIFIED	LF	475	DNR HATCHERY
	2003	UNSPECIFIED	LF	524	DNR HATCHERY
	2005	UPPER CHIPPEWA RIVER	LF	419	DNR HATCHERY
	2007	UPPER CHIPPEWA RIVER	LF	350	DNR HATCHERY
TCF	NR				
TH	1973	UNSPECIFIED	FI	575	DNR COOP PONDS
	1973	UNSPECIFIED	FY	94250	DNR HATCHERY
	1974	UNSPECIFIED	FI	2317	DNR COOP PONDS
	1976	UNSPECIFIED	FI	686	DNR COOP PONDS
	1977	UNSPECIFIED	FI	7757	DNR COOP PONDS
	1978	UNSPECIFIED	FI	722	DNR COOP PONDS
	1979	UNSPECIFIED	FI	2500	DNR COOP PONDS
	1980	UNSPECIFIED	FI	3493	DNR COOP PONDS
	1980	UNSPECIFIED	FY	32400	DNR HATCHERY
	1983	UNSPECIFIED	FI	3000	DNR COOP PONDS
	1985	UNSPECIFIED	FI	4420	DNR COOP PONDS
	1987	UNSPECIFIED	FI	3878	DNR COOP PONDS
	1987	UNSPECIFIED	FI	1939	DNR HATCHERY
	1988	UNSPECIFIED	FI	86	DNR COOP PONDS
	1989	UNSPECIFIED	FI	377	DNR COOP PONDS
	1989	UNSPECIFIED	FI	7000	DNR HATCHERY
	1990	UNSPECIFIED	FY	101250	DNR HATCHERY
	1991	UNSPECIFIED	FI	215	DNR COOP PONDS
	1991	UNSPECIFIED	FI	2140	DNR HATCHERY
	1992	UNSPECIFIED	FI	4055	DNR HATCHERY
	1992	UNSPECIFIED	FY	82750	DNR HATCHERY
	1993	UNSPECIFIED	FI	1385	DNR COOP PONDS
	1995	UNSPECIFIED	FY	200000	DNR HATCHERY
	1996	UNSPECIFIED	FY	82400	DNR HATCHERY
	1997	UNSPECIFIED	FY	334000	DNR HATCHERY
	1997	UNSPECIFIED	LF	1500	DNR HATCHERY
	1998	UNSPECIFIED	FY	56750	DNR HATCHERY
	1999	UNSPECIFIED	LF	1000	DNR HATCHERY
	2000	UNSPECIFIED	FY	42100	DNR HATCHERY
	2001	UNSPECIFIED	LF	850	PRIVATE HAT.
WSL	NR				
WO	NR				

*BL was stocked from 1982-1996 by an unspecified source (F. Pratt, personal communication).